

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:59:47 ; Search time 31.6667 Seconds
(without alignments) 89.674 Million cell updates/sec

Title: US-09-761-636A-10
Perfect score: 50
Sequence: 1 CSVPLITSVC 9

Scoring table: BLOSUM62
Gapox 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL 25:
 1: sp_archea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mmc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_tvirus:
 16: sp_bacteriap:
 17: sp_archeap:

Q9say7 dioscorea t
Q9tkf2 asteromyrtu
Q9tkg1 calothamnus
P70804 azotobacter
Q07624 rous sarcom
Q9ps68 gallus gallus Gall
Q67113 influenaviru
Q15890 homo sapien
Q15898 homo sapien
Q15899 homo sapien
Q9tkd9 pericalyxyma
Q9rij4 mus musculus
Q9c535 arabisopsis
Q9c536 ratus norvegicus
Q9k107 hepatitis b virus
Q9K4M6 staphylococ
Q15999 homo sapien
Q9tkd9 pericalyxyma
Q9c535 arabisopsis
Q5184 ratus norvegicus
Q45615 bacillus suis
Q32560 escherichia
Q9x3K1 prochlorococcus
P83152 anaerena sp
Q7x4Q5 nodularia s
Q8iv87 homo sapien
Q92032 lytechinus

ALIGNMENTS

RESULT 1
 Q8GMM5 ID Q8GMM5 PRELIMINARY; PRT; 8 AA.
 AC Q8GMM5; DT 01-MAR-2003 (T=EMBLrel. 23, Created)
 AC Q8GMM5; DT 01-MAR-2003 (T=EMBLrel. 23, Last sequence update)
 AC Q8GMM5; DT 01-JUN-2003 (T=EMBLrel. 24, Last annotation update)

DE Transposase (Fragment).
 GN TNP17.
 OS Acinetobacter sp. BM3.
 OC Plasmid pKLH207.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OC NCBI_TaxID-106395;
 RN [1] _SEQUENCE FROM N.A.
 RP STRAIN=BW3; PLASMID=pKLH207;
 RA Kholidii G.Y., Mindin S.Z., Gorlenko Z.M., Gorlenko Z.M.,
 RA Nikiforov V.G.;
 RT "pKLH2-like aberrant transposons and possible mechanisms of their
 dissemination";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2] _SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC STRAIN=BW3; PLASMID=pKLH207;
 RA Kholidii G.Y., Mindin S.Z., Gorlenko Z.M., Gorlenko Z.M.,
 RA Petrova M.A., Nikiforov V.G.;
 RA "A young family of transposable adaptive DNA segments identified in
 the Acinetobacter genus";
 RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RL Submitted (AJ250234; CAC0784; 1-;
 DR EMBL; AJ446856; CAD31078; 1-;
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_CER
 SQ SEQUENCE 8 AA; 911 MW; 2D71B2DC1A73774 CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	20	40.0	8 2 Q8GMM5	Q8gmm5 acinetobact
2	18	36.0	9 10 Q9fxL0	Q9fxl0 lilium longiflorum
3	17	34.0	7 13 Q8jj20	Q8jj20 gallus gallus Gall
4	17	34.0	7 13 Q42564	Q42564 fugu rubripinnatus
5	17	34.0	8 15 Q85562	Q85562 moloney murine leukaemia virus
6	17	34.0	9 11 Q8cg13	Q8cg13 mus musculus
7	16	32.0	8 2 Q8bpX4	Q8kpX4 microcystis
8	16	32.0	8 2 Q849P4	Q849p4 salmonella
9	16	32.0	8 4 Q9YAX6	Q9YAX6 homo sapiens
10	16	32.0	8 4 Q16468	Q16468 homo sapiens
11	16	32.0	8 10 Q8Lj802	Q8Lj802 zea mays (mexican corn)
12	16	32.0	9 6 Q9TRUT	Q9TRUT bos taurus
13	16	32.0	9 11 Q15953	Q15953 mus musculus
14	15	30.0	8 2 Q56140	Q56140 streptococcus
15	15	30.0	8 8 Q9TKES	Q9TKES leptospirermu
16	15	30.0	8 8 Q9MD43	Q9md43 rattus norvegicus

Query Match Score 20; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1e+06;

	Matches	4 ; Conservative	0 ; Mismatches	1 ; Indels	0 ; Gaps	0 ;	
Qy	4 PITSY 8						042564 PRELIMINARY; PRT; 7 AA.
Db	2 PLTQV 6						ID 042564; AC 042564; DT 01-JAN-1998 (TREMBrel. 05, Created) DT 01-JAN-1998 (TREMBrel. 05, Last sequence update) DT 01-JUN-2003 (TREMBrel. 24, Last annotation update) DE Truncated voltage-gated sodium channel alpha subunit (Fragment). GN SCN8A.
RESULT 2							
Q9PXL0	PRELIMINARY;	PRT;	9 AA.				OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes). OS Buiaryota; Metazoa; Chordata; Craniata; Buteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Neoteleosteoi; OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; OC Tetradontoidae; Tetraodontidae; Takifugu. NCBI_TaxID=31033; [1]
Q9PXL0	PRELIMINARY;	PRT;	9 AA.				RN SEQUENCE FROM N.A. MEDLINE=9741476; PubMed=9295353;
AC							RX RA Plummer N.W., McBurney M.W., Meissler M.H.; "Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells."; RT RL J. Biol. Chem., 272:24008-24015(1997).
DT	01-MAR-2001 (TREMBrel. 16, Created)						DR EMBL; 097673; AAB0916.1; -.
DT	01-MAR-2001 (TREMBrel. 16, Last sequence update)						DR GO:0005216; F:ion channel activity; IBA.
DT	01-MAR-2001 (TREMBrel. 16, Last annotation update)						KW Ionic channel.
DE	LIN8 Protein (Fragment).						FT NON_TER 1 1
GN	LIN8.						SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
OS	Lilium longiflorum (Trumpet lily).						Query Match 34.0%; Score 17; DB 13; Length 7; Best Local Similarity 71.4%; Pred. No. 1e+06; Mismatches 0; Indels 2; Gaps 1;
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.						Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
OC	"Lilium longiflorum LIN8 gene, promoter region and partial sequence."						Qy 3 VPLTSVC 9
OX	"Lilium longiflorum LIN8 gene, promoter region and partial sequence."						Db 1 VPL--VC 5
RN	[1]						
RP	SEQUENCE FROM N.A.						
RA	Uefuji H., Hinomoto;						
RA	"Lilium longiflorum LIN8 gene, promoter region and partial sequence."						
RT	"Lilium longiflorum LIN8 gene, promoter region and partial sequence."						
RT	Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.						
DR	EMBL: AB050937; BAB17856.1; -.						
FT	NON_TER 9 9 MW; 6F8BD76685A6C2CB CRC64;						
SQ	SEQUENCE 9 AA; 1021 MW;						
RESULT 3							
Q8JJ20	PRELIMINARY;	PRT;	7 AA.				RESULT 5 Q85562 PRELIMINARY; PRT; 8 AA.
Q8JJ20	PRELIMINARY;	PRT;	7 AA.				RN SEQUENCE FROM N.A. MEDLINE=8219891; PubMed=6281735;
AC	Q8JJ20;						RA Donoghue D.J., Hunter T.; RT "A generalized method of subcloning DNA fragments by restriction site recombination: Application to sequencing the amino-terminal region of the transforming gene of Gardar murine sarcoma virus."; RT NCBI_TaxID=11801; RN [2]
DT	01-OCT-2002 (TREMBrel. 22, Created)						RP SEQUENCE OF 4-8 FROM N.A. MEDLINE=8219891; PubMed=6281735;
DT	01-OCT-2002 (TREMBrel. 22, Last sequence update)						RA Donoghue D.J., Hunter T.; RT "A generalized method of subcloning DNA fragments by restriction site recombination: Application to sequencing the amino-terminal region of the transforming gene of Gardar murine sarcoma virus."; RT NCBI_TaxID=11801; RN [2]
DB	Extractacellular fatty acid binding protein (Fragment).						RP SEQUENCE FROM N.A. MEDLINE=8219891; PubMed=6281735;
GN	EXFABP.						RA Donoghue D.J., Hunter T.; RT "A generalized method of subcloning DNA fragments by restriction site recombination: Application to sequencing the amino-terminal region of the transforming gene of Gardar murine sarcoma virus."; RT NCBI_TaxID=11801; RN [2]
OS	Gallus gallus (Chicken).						RP SEQUENCE FROM N.A. MEDLINE=8219891; PubMed=6281735;
OC	Archosauria; Metazoa; Chordata; Craniata; Phasianidae; Galliformes; Gallinidae; Aves; Neognathae; Phasianinae;						RA Donoghue D.J., Hunter T.; RT "A generalized method of subcloning DNA fragments by restriction site recombination: Application to sequencing the amino-terminal region of the transforming gene of Gardar murine sarcoma virus."; RT NCBI_TaxID=11801; RN [2]
OC	Gallus.						RP SEQUENCE FROM N.A. MEDLINE=8219891; PubMed=6281735;
RN	[1]						RA Donoghue D.J., Hunter T.; RT "A generalized method of subcloning DNA fragments by restriction site recombination: Application to sequencing the amino-terminal region of the transforming gene of Gardar murine sarcoma virus."; RT NCBI_TaxID=11801; RN [2]
RP	SEQUENCE FROM N.A.						
RA	TISSUE=Blood;						
RA	Wang Q., Li N., Li H.;						
RA	"Cloning and sequencing of 3' UTR of EXFABP gene in chicken."						
RA	Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.						
DR	EMBL; AF487519; AAL96665.1; -.						
FT	NON_TER 1 1						
SQ	SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BEBBB70 CRC64;						
RESULT 4							
Qy	1 CSV 3						Query Match 34.0%; Score 17; DB 15; Length 8; Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;
Db	2 CSV 4						Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6							
Q8CGI3	PRELIMINARY;	PRT;	9 AA.				
ID Q8CGI3 ; AC Q8CGI3 ; DT 01-MAR-2003 (TREMBLrel. 23, Created) DT 01-JUN-2003 (TREMBLrel. 23, Last sequence update)							
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)							
DE Glutamate receptor ionotropic N-methyl D-aspartate-like 1A (Fragment).							
GN GRIN1A.							
OS Mus musculus (Mouse).							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. OX NCBI_TaxID=10530; [1]							
RN RP SEQUENCE FROM N.A.							
RC STRAIN=C5BL/6J; RA Wydner K.S.; Mohan Raj B.K.; Sciorra L.J.; Roginski R.S.; RT "The mouse orthologue of the human ionotropic glutamate receptor-like gene (GRIN1A) maps to mouse chromosome 9."; RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.							
EMBL; AF452417; AAC015648.1; -							
EMBL; AF62416; AAC015648.1; JOINED.							
DR MGD; MGI:107282; Grin1a.							
DR GO: GO:0004872; F:receptor activity; IEA.							
KW Receptor.							
FT NON_TER 1 1							
SQ SEQUENCE 9 AA; 1091 MW; 6A91233EB059C33B CRC64;							
Query Match 1 CSVP 4							
Best Local Similarity 50.0%; Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;							
RESULT 7							
Q8KPK4	PRELIMINARY;	PRT;	8 AA.				
ID Q8KPK4 ; AC Q8KPK4 ; DT 01-OCT-2002 (TREMBLrel. 22, Created) DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)							
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)							
DB Phycocyanin alpha subunit (Fragment).							
GN Microcystis sp. T96-1.							
OS Bacteria; Cyanobacteria; Chroococcales; Microcysts. OC NCBI_TaxID=198099; OX [1]							
RN RP SEQUENCE FROM N.A.							
RC STRAIN=bloom water sample T96-1; RA Baker J.A., Ertisch B., Neilan B.A., McKay D.B.; Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.							
EMBL; AY117046; AACM34719.1; -							
FT NON_TER 8 8							
SQ SEQUENCE 8 AA; F4DB01A73771A336 CRC64;							
Query Match 4 PLT 6							
Best Local Similarity 100.0%; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
RESULT 8							
Q84934	PRELIMINARY;	PRT;	8 AA.				
ID Q84934 ; AC Q84934 ; DT 01-JUN-2003 (TREMBLrel. 24, Created) DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)							
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
DE Pipp (Fragment).							
OS Salmonella derby.							
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.							
NCBI_TaxID=28144; OX [1]							
RN RP SEQUENCE FROM N.A.							
RC STRAIN=9813031; RA Markham P.F.; Amavisit P.; Lightfoot D.; Browning G.F.; RT "Variation between pathogenic serovars within <i>Salmonella</i> pathogenicity islands". RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.							
EMBL; AY144492; AAC049836.1; -							
FT NON_TER 8							
SQ SEQUENCE 8 AA; 861 MW; BPG5BDD451A04766 CRC64;							
Query Match 3 VPLTS 7							
Best Local Similarity 40.0%; Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;							
Qy DR							
Db 1 MPITN 5							
RESULT 9							
Q9Y4X6	PRELIMINARY;	PRT;	8 AA.				
ID Q9Y4X6 ; AC Q9Y4X6 ; DT 01-NOV-1999 (TREMBLrel. 12, Created) DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)							
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)							
DE Nuclear LIM interactor (Fragment).							
GN NLI.							
OS Homo sapiens (Human).							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo. NCBI_TaxID=9606; OX [1]							
RN RP SEQUENCE FROM N.A.							
RX MEDLINE=2010886; PubMed=10640831; RA Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S., Schrot A., Boedem J., Royer-Pokora B.; RT "Genomic structure, alternative transcripts and chromosome location of the human LIM domain binding protein gene LDB1." RT Cytogenet. Cell Genet. 87:119-124(1999). DR EMBL; AJ243097; CAB45408.1; -							
FT NON_TER 8							
SQ SEQUENCE 8 AA; 767 MW; ER6EBDDB862D5B6 CRC64;							
Query Match 1 CSVP 4							
Best Local Similarity 50.0%; Matches 2; Conservative 1; Mismatches 1; Indels 1; Gaps 0;							
Qy Db							
Db 5 CACP 8							
RESULT 10							
Q16468	PRELIMINARY;	PRT;	8 AA.				
ID Q16468 ; AC Q16468 ; DT 01-Nov-1996 (TREMBLrel. 01, Created) DT 01-May-1999 (TREMBLrel. 10, Last sequence update) DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)							

DE DNA for cosmid cC13-1134 PCR primer 1 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:92112868; PubMed=1309786;
 RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
 RA Burgess A.W.;
 RT "The purification of a Rap1 GTPase-activating protein from bovine
 brain cytosol."
 RL J. Biol. Chem. 267:1546-1553(1992).
 FT NON-TER 1 1
 FT NON-TER 1 1
 SQ SEQUENCE 9 AA; 1063 MW; 89EDA77B47604B5A CRC64;

Query Match 32.0%; Score 16; DB 6; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPVTSV 8
 Db 4 IVPFSV 9

RESULT 13
 O35953 PRELIMINARY; PRT; 9 AA.
 ID O35953
 AC O35953;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
 GN SCN8A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=III;
 RX MEDLINE:97442476; PubMed=9295353;
 RA Plummer N.W., McBurney M.W., Maisler M.H.;
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
 two-domain protein in fetal brain and non-neuronal cells."
 RL J. Biol. Chem. 272:24008-24015(1997).
 DR MGII:103169; Scn8a.
 GO:GO-0007288; P:adult walking behavior; IMP.
 KW Ionic channel.
 DR GO:0007288;
 FT NON-TER 1 1
 SQ SEQUENCE 9 AA; 899 MW; 22D92865B735B737 CRC64;

Query Match 32.0%; Score 16; DB 11; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPVTSV 6
 Db 1 VPVS 4

RESULT 14
 O56140 PRELIMINARY; PRT; 8 AA.
 ID O56140
 AC O56140;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Stp6 protein (Fragment).
 GN Stp6.
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=1308;
 RN [1]

RESULT 12
 Q9TRU7 PRELIMINARY; PRT; 9 AA.
 AC Q9TRU7
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE GAP-3, GTPase-activating protein (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.

RP SEQUENCE FROM N.A.
 RC STRAIN=ST11;
 RX MEDLINE=95047254; PubMed=7958782;
 RA Constable A., Mollet B.;
 RT "Isolation and characterisation of promoter regions from *Streptococcus thermophilus*."
 RL FEMS Microbiol. Lett. 122:85-90(1994).
 DR EMBL; X78210; CAA55045.1; -.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;
 Query Match Score 15; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SVP 4
 Db 4 SVP 6

RESULT 15
 Q9TKES PRELIMINARY; PRT; 8 AA.
 ID Q9TKES;
 AC Q9TKES;
 DT 01-MAY-2000 (TREMBUREL 13, Created)
 DT 01-MAY-2000 (TREMBUREL 13, Last sequence update)
 DT 01-JUN-2003 (TREMBUREL 24, Last annotation update)
 DE AtPB (Fragment).
 GN AtPB.
 OS *Lepiospermum erubescens*.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Leptospermum.
 NCBI_TaxID=106049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae)." ;
 RL Aust. J. Bot. 48:0-0(2000).
 DR EMBL; AF184690; AA073860.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 876 MW; EC0A1B1B764405056 CRC64;
 Query Match Score 15; DB 8; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 PLTS 7
 Db 5 PRTS 8

Search completed: September 5, 2004, 11:05:42
 Job time : 32.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:56:37 ; Search time 37.3333 Seconds

(without alignments)

68.114 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSYPLTSVC 9

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

231240

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: GeneseqP1980s:*

2: GeneseqP1990s:*

3: GeneseqP2000s:*

4: GeneseqP2001s:*

5: GeneseqP2002s:*

6: GeneseqP2003abs:*

7: GeneseqP2003bs:*

8: GeneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	
1	50	100.0	9	4 AAU04529	Aau04529 VEGF base	XX
2	37	74.0	9	5 ABJ04424	Abj04424 Stem cell	PD
3	32	64.0	9	5 ABG34948	Abg34948 Human bon	XX
4	30	60.0	7	6 ABJ37356	Abj37356 G-protein	PF
5	30	60.0	7	6 ABJ37436	Abj37436 G-protein	XX
6	30	60.0	9	5 ABB05266	Abb05266 Vascular	PR
7	28	50.0	9	7 ADC44660	Adc44660 Endotheli	PR
8	27	54.0	9	2 AAW45666	Aaw45666 HBV X 69	XX
9	27	54.0	9	2 AAY46691	Aay46691 Immunogen	PA
10	27	54.0	9	5 ABP54842	Abp54842 Alpha-IIb	PA
11	26	52.0	7	7 ADB79577	Adb79577 Parapoxv	PI
12	26	52.0	9	4 AAU03756	Aau03756 Cyclic pe	XX
13	26	52.0	9	5 ABP54826	Abp54826 Alpha-IIb	DR
14	26	52.0	9	5 ABP54835	Abp54835 Alpha-IIb	XX
15	26	52.0	9	5 ABP54823	Abp54823 Alpha-IIb	PT
16	26	52.0	9	6 ABR75294	Abr75294 Biologica	PT
17	25	50.0	7	3 AAB51972	Aab51972 Human sec	PT
18	25	50.0	8	5 ABJ04484	Abj04484 HUVEC cel	XX
19	25	50.0	9	2 AAY48844	Aay48844 Membrane	PS
20	25	50.0	9	3 AAY64300	Aay64300 Cadherin	XX
21	25	50.0	9	4 AAU03747	Aau03747 Cyclic pe	CC
22	25	50.0	9	5 ABJ04420	Abj04420 Bone marr	CC
23	25	50.0	9	5 ABJ04630	Abj04630 Bone marr	CC
24	25	50.0	9	5 ABJ04417	Abj04417 Stem cell	CC
25	25	50.0	9	7 ADC44658	Adc44658 Endotheli	CC

ALIGNMENTS

RESULT 1

AAU04529

ID

AAU04529 standard; Peptide; 9 AA.

XX

AC

AAU04529;

XX

DT

26-SSP-2001 (first entry)

XX

DE

VEGF based monocyclic peptide 7.

XX

KW

Human; VEGF; vascular endothelial growth factor; angiogenesis;

XX

KW

neovascularisation; lymphangiogenesis; psoriasis; tumour;

XX

KW

diabetes induced neovascular sequelae; rheumatoid arthritis;

XX

KW

diabetic retinopathy; chronic inflammation; cyclic.

XX

FT

Key Disulfide-bond 1..9

/note= "This bond cyclises the peptide"

XX

FT

FT

W0200152875-A1.

XX

XX

26-JUL-2001.

XX

XX

18-JAN-2001; 2001WO-US001533.

XX

XX

18-JAN-2000; 2000US-0176293P.

XX

16-MAY-2000; 200001S-0204590P.

XX

XX

(LUDWIG INST CANCER RES.

XX

PA

peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioblastic malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced reovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CSYPLTSVC 9	50	4	Prod. No. 1.4e+06;	9 AA.	0	0	0	0	0	1
Db	1 CSYPLTSVC 9	0	0			0	0	0	0	0	0

XX Sequence 9 AA;

Query	Match	Score	Length	DB	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	No.
QY	1 CS										

AC ABB05266;
 XX 29-AUG-2003 (revised)
 DT 04-APR-2002 (first entry)

XX Vascular endothelial growth factor binding peptide V-20 SEQ ID NO:98.
 XX Human; tumour necrosis factor alpha; TNF-alpha; VEGF; detergent; stain;
 KW bacteriophage; phage library; vascular endothelial growth factor;
 KW collar soil; polyurethane; egg; tea; hair; skin; cleaning composition.
 XX unidentified bacteriophage.
 OS unidentified.
 XX WO200179479-A2.
 XX 25-OCT-2001.
 XX 11-APR-2001; 2001WO-US011811.
 PR 14-APR-2000; 2000US-0197259P.
 XX (GEMV) GENENCOR INT INC.
 PA Estell DA, Murray CJ, Tijerina P, Chen Y;
 PI DR, 2002-139323/18.
 XX Screening ligand library comprises allowing binding of ligand with anti-target,
 PT contacting unbound ligands with selected target to form target-bound ligand complex and identifying target bound ligands on the complex.
 PT XX
 PS Claim 22; Page 28; 51PP; English.
 XX The present invention describes a method for screening a ligand library
 CC (LL). The method comprises: (a) contacting the LL with an anti-target
 CC (AT) to allow the ligands to bind to the AT; (b) separating unbound
 CC ligands; (c) contacting the unbound ligands with a selected target (T) to
 CC allow binding of unbound ligands to (T) to form a (T)-bound ligand
 complex (C); (d) separating (C) from ligands which do not bind (T); and
 CC (e) identifying (T)-bound ligands on (C). The method can be used for
 CC screening a ligand library e.g., a library of peptides, polypeptides,
 CC non-polypeptides or oligonucleotides. A ligand (L) identified by the
 CC method can be used in a cleaning, therapeutic or personal care
 CC application. The method is preferably useful for identifying peptides
 CC useful in cleaning compositions, which involves contacting peptide
 CC library with AT such as fabric, ceramic, glass, stainless steel or
 CC plastic; separating unbound AT peptides; contacting unbound AT peptides
 CC with target which is a stain such as porphyrin derived stain, tannin
 CC derived stain, carotenoid pigment derived stain, anthocyanin pigment
 CC derived stain, soil-based derived stain, oil-based derived stain, and
 CC human body stain, to allow unbound peptide to bind with the stain to form
 CC a stain-bound peptide complex and identifying the stain-bound peptide on
 CC the stain-bound peptide complex. A selective targeting method for
 CC screening a library of ligands that bind to a target may be used to
 CC identify ligands that bind to a target under harsh conditions. The
 CC selective targeting method may be used to screen and identify a ligand
 CC useful for therapeutic intervention, e.g., a library of ligands may be
 CC screened to identify a tumour-bound ligand. The selective targeting
 CC method may be used to identify cell type specific surface molecules.
 CC Preferred anti-targets include one or more different cell types, cells in
 CC different states, or cells that do not display the surface molecule.
 CC ABB05232 to AB05346 represent phage-peptides ligands which are used in
 CC the exemplification of the present invention. (Updated on 29-Aug-2003 to
 CC standardise OS field)
 XX Sequence 9 AA;

Db :|:||| 1 CMAPTSKVC 9

RESULT 7
 ADC44660 ID ADC44660 standard; peptide; 9 AA.
 XX
 AC ADC44660;
 XX 18-DEC-2003 (first entry)
 DT DB Endothelial cell binding peptide SEQ ID NO:389.
 XX
 KW endothelial cell binding protein; ECBP; anti-tumour; cytostatic;
 KW vasoconstrictive; antipsoriatic; dermatological; ophthalmological;
 KW antibacterial; antiarthritic; vulnerary; antiulcer; antiinflammatory;
 KW antibacterial; gynaecological; angiogenesis.
 XX
 OS Synthetic.
 XX
 PN WO2003037172-A2.
 XX 08-MAY-2003.
 PD XX 01-NOV-2002; 2002WO-US035258.
 PF XX 01-NOV-2001; 2001US-0334822P.
 PR XX (GPCB-) GPC BIOTECH INC.
 PI Gyaris J, Lamphere L, Morris AJ, Tsaioun K;
 XX DR WO2003-482072/45.
 PR XX
 PT Novel synthetic or recombinant polypeptide useful for promoting, reducing
 PT proliferation and/or migration of endothelial cells, and for modulating
 PT angiogenesis, has endothelial cell binding protein sequences.
 XX
 PS Claim 3; SEQ ID NO 389; 12PP; English.
 XX
 CC The invention relates to a novel isolated, synthetic or recombinant
 CC peptide or polypeptide which includes one or more endothelial cell
 CC binding protein (ECBP) sequences. A peptide of the invention has anti-
 CC tumour, cytostatic, vasoconstrictive, antipsoriatic, dermatological,
 CC opthalmological, antidiabetic, antiarthritic, vulnerary, antiulcer,
 CC antiinflammatory, antibacterial, and gynaecological activity. The peptide
 CC is useful for promoting, reducing the proliferation and/or migration of
 CC endothelial cells, by treating the cells with an ECBP agonist, which is
 CC preferably the peptide, to promote proliferation and/or migration of the
 CC treated cells, and for reducing or promoting angiogenesis, by treating
 CC the cells with an ECBP antagonist, which is preferably the peptide of the
 CC invention. A peptide of the invention is also useful for manufacturing a
 CC medicament for promoting angiogenesis, by admixing an ECBP agonist or
 CC ECBP antagonist to promote or reduce angiogenesis at one or more sites in
 CC a treated mammal. The medicament is useful for promoting or reducing
 CC angiogenesis. ECBP sequences are useful to alter the infectivity spectrum
 CC of a viral particle. The present sequence represents an ECBP of the
 CC invention.
 XX Sequence 9 AA;

SQ Query Match 56.0%; Score 28; DB 7; Length 9;
 Best Local Similarity 33.3%; Pred. No. 1.4e+06;
 Matches 3; Mismatches 3; Indels 0; Gaps 0;

Db 1 CDLPTSRIC 9

RESULT 8
 AAW45666

QY 1 CSVPLTSVC 9
 | :|:||| 1 CDLPTSRIC 9

Query Match 60.0%; Score 30; DB 5; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1.4e+06;
 Matches 2; Mismatches 3; Indels 0; Gaps 0;

ID	AAW45666	standard; peptide; 9 AA.	XX	XX	XX	DT 01-DEC-1999 (first entry)
AC	AAW45666;		XX	XX	DE	Immunogenic peptide having a human leukocyte antigen binding motif #1302.
DT	27-AUG-2003 (revised)		XX	XX	KW	Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
DT	09-JUN-1998 (first entry)		XX	XX	KW	
DE	HBV X 69 peptide with binding affinity for HLA-A3-like molecules.		XX	XX	KW	
XX	HLA molecule; cytotoxic T cell; immunogenic peptide; binding affinity; HLA-A3 supermolecule; tumour; infection; parasite; CTL; antigen; HIV protein; HBV; hepatitis b virus.		XX	XX	KW	
XX	Synthetic.		OS	OS	OS	
OS	Repatitis B virus.		OS	OS	Homo sapiens.	
XX			XX	PN	WO9945954 A1.	
PN	WO9733602-A1.		XX	PD	16-SEP-1999.	
XX			XX	PP	13-MAR-1998; 98WO-US005039.	
PD	18-SEP-1997.		XX	PR	13-MAR-1998; 98WO-US005039.	
XX			XX	PA	(EPIM-) EPIMMUNE INC.	
PP	10-MAR-1997; 97WO-US003778.		XX	PI	Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S; PI; 1999-551214/46.	
XX			XX	DR		
PR	11-MAR-1996; 96US-0013113P.		XX	PT	New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases.	
XX			XX	PS	Claim 1; Page 81; 150pp; English.	
PA	(CYTE-) CYTEL CORP.		XX	CC	AAV48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A2.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans), e.g., prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above	
XX			XX	PS	Sequence 9 AA;	
PI	Sette A, Chestnut RW, Sidney J;		XX	CC	Sequence 9 AA;	
XX	DR; 1997-470637/43.		XX	CC	Score 27; DB 2; Length 9;	
XX			XX	CC	Best Local Similarity 57.1%; Pred. No. 1.4e+06;	
PT	Inducing cytotoxic T cell response against specific antigen - using immunogenic peptide with binding affinity for HLA-A3-like molecules, to treat or prevent tumours and infections by virus, parasites etc.		XX	Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	Qy 1 CSVPTS 7 : Db 1 CALPTS 7	0;
PT			XX	XX	RESULT 10 ABP54842 ID ABP54842 standard; peptide; 9 AA.	
PT			XX	XX	ABP54842; XX	
XX			XX	XX	08-JAN-2003 (first entry)	
PS	Example 1; Page 37; 79pp; English.		XX	XX		
XX	This sequence represents an immunogenic peptide with binding affinity for HLA-A3-like molecules. A cytotoxic T cell (CTL) response against a particular antigen (Ag) is induced in a patient by contacting a CTL with an immunogenic peptide of 9-15 amino acids which binds to at least two HLA-A3-like molecules with a dissociation constant less than 500 nM and induces a cytotoxic T cell response. The immunogenic peptide has a sequence of 9 amino acids, comprising a binding motif, with from the N-to C-termini: primary anchor sites (PAR) at positions 2 (selected from Ala, Leu, Ile, Val, Met, Ser or Thr) and 9 (Arg or Lys) and at least one secondary anchor sites (SAR), i.e. Tyr, Phe or Trp at positions 3, 6 or 7 and/or Pro at position 8. The immunogenic peptides are used in peptide based vaccines and therapeutic compositions, for treating viral, parasitic or fungal diseases or cancer, e.g. prostatic cancer, hepatitis B or C, renal or cervical carcinoma, lymphoma, cytomegalovirus infection or condyloma acuminatum. They can also be used to elicit a CTL response in vitro for subsequent return of the cells to the patient, e.g. where the patient does not respond to peptide vaccines or other therapies. Selection of specific residues for PAR and SAR results in higher binding affinity and thus increased immunogenicity. (Updated on 27-AUG-2003 to correct OS field.)					
XX	Sequence 9 AA;		XX	XX	Score 27; DB 2; Length 9;	
Query Match	54.0%; Score 27; DB 2; Length 9;		XX	XX	Best Local Similarity 57.1%; Pred. No. 1.4e+06;	
Best Local Similarity	57.1%; Pred. No. 1.4e+06;		XX	Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	Qy 1 CSVPTS 7 : Db 1 CALPTS 7	0;
Matches	2; Mismatches 1; Indels 0; Gaps 0;		XX	XX	RESULT 10 ABP54842 ID ABP54842 standard; peptide; 9 AA.	
Qy	1 CSVPTS 7		XX	XX	ABP54842; XX	
Db	1 CALPTS 7		XX	XX	08-JAN-2003 (first entry)	

DB Alpha-IIb beta-3 integrin activating peptide.
 XX Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61; coagulant; vulnerary;
 KW glycoprotein IIb/IIIa; von Willebrand disease; autoimmune disease.
 KW cyclic
 KW
 OS Synthetic.
 XX
 FF Key Location/Qualifiers
 FT Disulfide-bond 1..9
 PT Region 3..5 /note= "binding motif, region specifically described in
 FF Claim 1"
 XX WO2002072619-A1.
 XX PD 19-SEP-2002.
 XX PFF 12-MAR-2002; 2002WO-FF0000193.
 XX PR 12-MAR-2001; 2001FI-00000492.
 XX (CTTC) CTT CANCER TARGETING TECHNOLOGIES OY.
 XX PI Koivunen E, Gahmberg CG;
 XX DR WPI; 2002-750482/81.
 XX New alphaIIb beta3 integrin activating peptides useful for manufacturing
 PT compositions for treating or preventing thrombotic or bleeding
 PT disorders, e.g. von Willebrand disease, and in wound healing and tissue
 PT regeneration.
 XX Disclosure; Page 12; 34pp; English.
 XX The present sequence is that of a novel alpha-IIb beta-3 integrin
 CC (glycoprotein IIb/IIIa or CD41/CD61) activating peptide. This cyclic
 peptide comprises a consensus binding motif (Val-Pro-Trp) and was
 CC identified by focusing a phage library screening on integrin ligands
 CC which are not blocked by a GRGS peptide. The VWF motif is present in the
 CC A3-domain of von Willebrand factor (vWF), suggesting that vWF is an
 CC activator of the alpha-IIb beta-3 complex, enabling stable platelet-vWF
 CC interaction. The invention relates to the use of novel peptides (see
 CC ABP4823-25) comprising the consensus binding motif as pharmaceuticals
 CC for the treatment of thrombotic diseases and bleeding disorders,
 CC including von Willebrand disease, and in artificial tissue transplants to
 CC aid in wound healing and tissue regeneration (all claimed).
 XX Sequence 9 AA:
 SQ 54.0%: Score 27; DB 5; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1.4e+06;
 Matches 1; Mismatches 4; Indels 0; Gaps 0;
 Best Local Similarity 52.0%; Score 26; DB 7; Length 7;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CSVPITSCV 9
 DB 1 CDVPMRDLC 9
 RESULT 11
 ADB79677
 ID ADB79677 standard; peptide; 7 AA.
 XX AC ADB79677;
 XX DT 04-DEC-2003 (first entry)
 XX DE Parapoxvirus ORF 100 C-terminal peptide.
 XX KW viricide; anti-HIV; hepatotropic; antiinflammatory; cytosstatic;
 KW vulnerary; antiasthmatic; antiallergic; dermatological; antidiabetetic;
 KW immunosuppressive; antirheumatic; antiarthritic; thymomimetic;
 KW protozoacide; amoebicide; antibacterial; gene therapy; virus;
 KW

RW viral infections; non-viral infections; proliferative disease;
 KW inflammatory disease; allergic disease; autoimmune disease.
 KW Parapoxvirus.
 XX OS WO2003006654-A2.
 XX PN WO2003006654-A2.
 XX PD 23-JAN-2003.
 XX XX 12-JUN-2002; 2002WO-EP006440.
 XX PR 13-JUN-2001; 2001INZ-00512341.
 XX PA (FARB) BAYER AG.
 XX PI Weber O, Friederichs SM, Siegling A, Schlaupp T, Mercer AA;
 XX PI Fleming SB;
 XX DR WPI; 2003-2211750/21.
 XX PT New polynucleotide and recombinant proteins of Parapoxvirus ovis, useful
 PT for manufacturing a medicament for treating virus related disease, viral
 PT infections, non-viral infections, proliferative disease or inflammatory
 PT disease.
 XX PS Example 4; Page 37; 51pp; English.
 XX The invention relates to a novel purified and isolated polynucleotide
 CC (N1) of Parapoxvirus ovis (PPVO) comprising a nucleotide sequence (S1,
 CC not defined in the specification), or its complementary sequence,
 CC fragment or functional variant. A polynucleotide of the invention has
 CC virucide, anti-HIV, hepatotropic, antimicrobial, cytostatic,
 CC vulnerary, antiasthmatic, antiallergic, dermatological, antidiabetetic,
 CC immunosuppressive, antirheumatic, antiarthritic, thymomimetic,
 CC protozoacide, amoebicide, and antibacterial activity. The polynucleotides
 CC may have a use in gene therapy. The recombinant proteins encoded by the
 CC polynucleotides or recombinant viruses comprising a Vaccinia virus
 CC genome and fragments of a PPVO genome are useful for manufacturing
 CC pharmaceutical compositions for treating virus related disease (e.g.
 CC hepatitis papillomatosis, herpes virus infections, liver fibrosis, HIV
 CC infections or influenza), viral infections, non-viral infections (e.g.
 CC infections with mycobacteria, amoebiasis, amoeba or plasmodia),
 CC proliferative disease (e.g. cancer, leukemia, warts or other skin
 CC neoplasms), inflammatory disease (e.g. Crohn's disease, COPD, asthma or
 CC conditions related to healing of wounds), allergic disease, and/or
 CC autoimmune diseases (systemic lupus erythematosus, Sjogren's disease,
 CC Hashimoto's thyroiditis, rheumatoid arthritis or diabetes mellitus). The
 CC present sequence is used in the exemplification of the invention.
 XX Sequence 7 AA:
 SQ Sequence 7 AA;
 Query Match 52.0%; Score 26; DB 7; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 DE Cyclic peptide inhibitor of LFA-1/ICAM-1 interaction #33.
 XX KW Cyclc; lymphocyte function associated antigen-1; LFA-1; asthma;
 KW intracellular adhesion molecule; ICAM-1; inhibitor; leukaemia;
 KW haematopoietic neoplastic disease; myocardial infarction;

KW radiation injury; rheumatoid arthritis; lymphoma metastasis;
 KW retinoic acid syndrome; all-trans retinoic acid.
 XX Synthetic.
 OS
 XX WO200151508-A1.
 PN
 XX PD 19-JUL-2001.
 XX PF 16-JAN-2001; 2001WO-US001382.
 XX PR 14-JAN-2000; 2000US-00483550.
 PR 16-JAN-2001; 2001US-00760599.
 XX PA (SCTE-) SCI & TECHNOLOGY CORP @UNM.
 XX PI Larson RS;
 XX DR WPI; 2001-432906/46.
 XX PT Composition comprising a cyclic peptide inhibitor of lymphocyte function associated antigen-1 and intracellular adhesion molecule 1 interaction, for treating e.g. asthma and myocardial infarction.
 XX Example 2; Page 23; 58pp; English.
 CC The sequence represents the amino acid sequence of cyclic peptide inhibitor #33 of lymphocyte function associated antigen-1 and intracellular adhesion molecule (LFA-1/ICAM-1) interaction. A composition comprising a cyclic peptide inhibitor of LFA-1/ICAM-1 interaction is useful for treating haematopoietic neoplastic disease, myocardial infarction, radiation injury, asthma, rheumatoid arthritis or lymphoma metastasis. The composition is also useful for inhibiting in a subject the interaction between LFA-1 expressed on a leukocyte and ICAM-1 expressed on another cell, preventing retinoic acid syndrome in a subject receiving all-trans retinoic acid, inhibiting growth of leukaemia cells, inhibiting emigration of leukocytes from blood into tissue and screening a candidate compound for binding to ICAM-1
 XX Sequence 9 AA;
 Query Match Score 26; DB 4; Length 9;
 Best Local Similarity 33.3%; Pred. No. 1.4e+06;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 RESULT 14
 Qy 1 CSVPLTSCV 9
 DB 1 CALRMRSC 9
 ABP54835
 ID ABP54835 standard; peptide; 9 AA.
 AC ABP54835;
 XX DT 08-JAN-2003 (first entry)
 XX Alpha-IIb beta-3 activating peptide.
 DE Alpha-IIb beta-3 standard; peptide; 9 AA.
 XX ABP54826
 AC ABP54826
 XX DT 08-JAN-2003 (first entry)
 XX Alpha-IIb beta-3 activating peptide.
 DE Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61;
 KW glycoprotein IIb/IIIa; von Willebrand disease; coagulant; vulnerable;
 KW cyclic.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Disulfide-bond 1..9
 FT Region 3..5
 FT /note= "binding motif, region specifically described in
 FT Claim 1"
 XX PN WO200272619-A1.
 XX PD 19-SEP-2002.
 XX PR 12-MAR-2002; 2002WO-FI000193.
 XX PR 12-MAR-2001; 2001FI-00000492.

XX PR 12-MAR-2001; 2001FI-00000492.

XX XX (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY.

XX PA

XX PI Koivunen E, Gahmberg CG;

XX DR WPI; 2002-750482/81.

XX New alphaIIb beta3 integrin activating peptides useful for manufacturing PT a composition for treating or preventing thrombotic or bleeding PR disorders, e.g. von Willebrand disease, and in wound healing and tissue regeneration.

XX Disclosure; Page 12; 34pp; English.

XX The present sequence is that of a novel alpha-IIb beta-3 integrin CC glycoprotein IIb/IIIa or CD41/CD61 activating peptide. This cyclic peptide comprises a consensus binding motif (Val-Pro-Trp) and was identified by focusing a phage library screening on integrin ligands which are not blocked by a GRGDs peptide. The vWF motif is present in the A3-domain of von Willebrand factor (vWF), suggesting that vWF is an activator of the alpha-IIb beta-3 complex, enabling stable platelet-vWF interaction. The invention relates to the use of novel peptides (see ABP5483-25) comprising the consensus binding motif as pharmaceuticals for the treatment of thrombotic diseases and bleeding disorders, including von Willebrand disease, and in artificial tissue transplants to aid in wound healing and tissue regeneration (all claimed).

XX Sequence 9 AA;

XX Query Match 52.0%; Score 26; DB 5; Length 9;

XX Best Local Similarity 44.4%; Pred. No. 1.4e+06;

XX Matches 2; Mismatches 3; Indels 0; Gaps 0;

XX

Qy	1 CSVPLTSVC 9	Score 26;	DB 5;	Length 9;
	[: :]	Best Local Similarity	44.4%;	Pred. No. 1.4e+06;
Db	1 CAVPWGRLC 9	Matches	4;	Mismatches 5;
		Qy	1 CSVPLTSVC 9	Indels 0; Gaps 0;
		Db	1 CXVPWXXXC 9	

XX Sequence 9 AA;

XX

RESULT 15

ID ABP54823 standard; peptide; 9 AA.

XX AC ABP54823;

XX DT 08-JAN-2003 (first entry)

XX DS Alpha-IIb beta-3 integrin activating peptide.

XX KW Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61; coagulant; vulnerary; cyclic.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..9

FT Misc-difference 2

FT /note= "any amino acid residue"

FT Region 3..5

FT /note= "binding motif, region specifically described in Claim 1"

FT Misc-difference 6

FT /note= "any amino acid residue"

FT Misc-difference 7

FT /note= "any amino acid residue"

FT Misc-difference 8

FT /note= "any amino acid residue"

XX PN WO200272619-A1.

XX PD 19-SEP-2002.

XX

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OM protein - protein search, using sw mode!

Run on: September 5, 2004, 11:05:54 ; Search time 35.6667 Seconds
(w/o alignments) 79.502 Million cell updates/sec

Title: US-09-761-636A-10
Perfect score: 50
Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 119143

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpa/us07_pubcomb.pep:
2: /cgn2_6/ptodata/2/pubpa/fct_new_pub.pep:
3: /cgn2_6/ptodata/2/pubpa/us06_pub.pep:
4: /cgn2_6/ptodata/2/pubpa/us07_pubcomb.pep:
5: /cgn2_6/ptodata/2/pubpa/us07_pubcomb.pep:
6: /cgn2_6/ptodata/2/pubpa/pctus_pubcomb.pep:
7: /cgn2_6/ptodata/2/pubpa/us08_pub.pep:
8: /cgn2_6/ptodata/2/pubpa/us09_pub.pep:
9: /cgn2_6/ptodata/2/pubpa/us09a_pubcomb.pep:
10: /cgn2_6/ptodata/2/pubpa/us09c_pubcomb.pep:
11: /cgn2_6/ptodata/2/pubpa/us09c_pubcomb.pep:
12: /cgn2_6/ptodata/2/pubpa/us09_new_pub.pep:
13: /cgn2_6/ptodata/2/pubpa/us10a_pubcomb.pep:
14: /cgn2_6/ptodata/2/pubpa/us10b_pubcomb.pep:
15: /cgn2_6/ptodata/2/pubpa/us10c_pubcomb.pep:
16: /cgn2_6/ptodata/2/pubpa/us10_new_pub.pep:
17: /cgn2_6/ptodata/2/pubpa/us60_pub.pep:
18: /cgn2_6/ptodata/2/pubpa/us60_pubcomb.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	50	100.0	9	9	US-09-761-636A-10	Sequence 10, Appl
2	32	64.0	9	12	US-10-363-208-24	Sequence 24, Appl
3	30	60.0	9	9	US-09-832-23-98	Sequence 98, Appl
4	30	60.0	9	14	US-10-303-331-98	Sequence 98, Appl
5	28	56.0	9	14	US-10-286-457-389	Sequence 389, Appl
6	26	52.0	9	9	US-09-760-539-34	Sequence 34, Appl
7	26	52.0	9	14	US-10-254-446A-147	Sequence 147, Appl
8	25	50.0	8	12	US-10-462-452-480	Sequence 480, Appl
9	25	50.0	8	16	US-10-601-953-509	Sequence 609, Appl
10	25	50.0	8	16	US-10-322-266-481	Sequence 481, Appl
11	25	50.0	9	9	US-09-760-539-25	Sequence 25, Appl
12	25	50.0	9	14	US-10-006-869-3614	Sequence 3614, Appl
13	25	50.0	9	14	US-10-286-457-387	Sequence 387, Appl
14	25	50.0	9	15	US-10-395-032-1614	Sequence 3614, Appl
15	24	48.0	7	9	US-09-761-636A-11	Sequence 11, Appl

SEQUENCES

Result No.	Score	Query	Match	Length	DB ID	Description
1	50	100.0	9	9	US-09-761-636A-10	Sequence 10, Appl
2	32	64.0	9	12	US-10-363-208-24	Sequence 24, Appl
3	30	60.0	9	9	US-09-832-23-98	Sequence 98, Appl
4	30	60.0	9	14	US-10-303-331-98	Sequence 98, Appl
5	28	56.0	9	14	US-10-286-457-389	Sequence 389, Appl
6	26	52.0	9	9	US-09-760-539-34	Sequence 34, Appl
7	26	52.0	9	14	US-10-254-446A-147	Sequence 147, Appl
8	25	50.0	8	12	US-10-462-452-480	Sequence 480, Appl
9	25	50.0	8	16	US-10-601-953-509	Sequence 609, Appl
10	25	50.0	8	16	US-10-322-266-481	Sequence 481, Appl
11	25	50.0	9	9	US-09-760-539-25	Sequence 25, Appl
12	25	50.0	9	14	US-10-006-869-3614	Sequence 3614, Appl
13	25	50.0	9	14	US-10-286-457-387	Sequence 387, Appl
14	25	50.0	9	15	US-10-395-032-1614	Sequence 3614, Appl
15	24	48.0	7	9	US-09-761-636A-11	Sequence 11, Appl

ALIGNMENTS

Result No.	Score	Query	Match	Length	DB ID	Description
1	50	100.0	9	9	US-09-761-636A-10	Sequence 10, Application US/09761636A
2	32	64.0	9	12	US-10-363-208-140	Sequence 24, Application US/09761636A
3	30	60.0	9	9	US-09-835-430-249	Sequence 98, Application US/09761636A
4	30	60.0	9	14	US-10-277-292-349	Sequence 34, Application US/09761636A
5	28	56.0	9	15	US-10-280-340-249	Sequence 35, Application US/09761636A
6	28	56.0	9	12	US-09-335-430-349	Sequence 32, Application US/09761636A
7	26	52.0	9	14	US-10-277-292-249	Sequence 31, Application US/09761636A
8	26	52.0	9	12	US-10-280-340-464	Sequence 30, Application US/09761636A
9	24	48.0	9	15	US-10-107-532-250	Sequence 29, Application US/09761636A
10	24	48.0	9	15	US-10-107-532-256	Sequence 28, Application US/09761636A
11	24	48.0	9	15	US-10-107-532-257	Sequence 27, Application US/09761636A
12	24	48.0	9	15	US-10-107-532-778	Sequence 26, Application US/09761636A
13	24	48.0	9	15	US-10-107-532-792	Sequence 25, Application US/09761636A
14	24	48.0	9	15	US-10-107-532-809	Sequence 24, Application US/09761636A
15	24	48.0	9	15	US-10-107-532-1314	Sequence 23, Application US/09761636A
16	24	48.0	9	15	US-10-107-532-1319	Sequence 22, Application US/09761636A

RESULTS

Result No.	Score	Query	Match	Length	DB ID	Description
1	50	100.0	9	9	US-09-761-636A-10	Sequence 1, CSVPLTSVC 9
2	32	64.0	9	12	US-10-363-208-140	Sequence 2, CSVPLTSVC 9
3	30	60.0	9	9	US-09-835-430-249	Sequence 3, CSVPLTSVC 9
4	30	60.0	9	14	US-10-277-292-349	Sequence 4, CSVPLTSVC 9
5	28	56.0	9	15	US-10-280-340-249	Sequence 5, CSVPLTSVC 9
6	28	56.0	9	12	US-09-335-430-349	Sequence 6, CSVPLTSVC 9
7	26	52.0	9	14	US-10-277-292-249	Sequence 7, CSVPLTSVC 9
8	26	52.0	9	12	US-10-280-340-464	Sequence 8, CSVPLTSVC 9
9	24	48.0	9	15	US-10-107-532-250	Sequence 9, CSVPLTSVC 9
10	24	48.0	9	15	US-10-107-532-256	Sequence 10, CSVPLTSVC 9
11	24	48.0	9	15	US-10-107-532-257	Sequence 11, CSVPLTSVC 9
12	24	48.0	9	15	US-10-107-532-778	Sequence 12, CSVPLTSVC 9
13	24	48.0	9	15	US-10-107-532-792	Sequence 13, CSVPLTSVC 9
14	24	48.0	9	15	US-10-107-532-809	Sequence 14, CSVPLTSVC 9
15	24	48.0	9	15	US-10-107-532-1314	Sequence 15, CSVPLTSVC 9

RESULTS 2

Result No.	Score	Query	Match	Length	DB ID	Description
1	50	100.0	9	9	US-09-761-636A-10	Query 1, CSVPLTSVC 9
2	32	64.0	9	12	US-10-363-208-24	Query 2, CSVPLTSVC 9
3	30	60.0	9	9	US-09-835-430-249	Query 3, CSVPLTSVC 9
4	30	60.0	9	14	US-10-277-292-349	Query 4, CSVPLTSVC 9
5	28	56.0	9	15	US-10-280-340-249	Query 5, CSVPLTSVC 9
6	28	56.0	9	12	US-09-335-430-349	Query 6, CSVPLTSVC 9
7	26	52.0	9	14	US-10-277-292-249	Query 7, CSVPLTSVC 9
8	26	52.0	9	12	US-10-280-340-464	Query 8, CSVPLTSVC 9
9	24	48.0	9	15	US-10-107-532-250	Query 9, CSVPLTSVC 9
10	24	48.0	9	15	US-10-107-532-256	Query 10, CSVPLTSVC 9
11	24	48.0	9	15	US-10-107-532-257	Query 11, CSVPLTSVC 9
12	24	48.0	9	15	US-10-107-532-778	Query 12, CSVPLTSVC 9
13	24	48.0	9	15	US-10-107-532-792	Query 13, CSVPLTSVC 9
14	24	48.0	9	15	US-10-107-532-809	Query 14, CSVPLTSVC 9
15	24	48.0	9	15	US-10-107-532-1314	Query 15, CSVPLTSVC 9

PATENTS

SEQ ID No	Length	Type	Organism
10	9	PRT	Homo sapiens
11	9	PRT	Homo sapiens
12	9	PRT	Homo sapiens
13	9	PRT	Homo sapiens
14	9	PRT	Homo sapiens
15	9	PRT	Homo sapiens

PATENT INFORMATION

Patent No.	Application Number	Priority Application Number	Prior Filing Date	Current Application Number	Number of SEQ ID NOS:	Software: PatentIn version 3.0
US2002006518A1	US/09761636A	US 60/176,93	2000-01-18	US 60/176,93	34	PatentIn version 3.0
US-09-761-636A-10	US/09761636A	US 60/176,93	2000-05-16	US 60/176,93	34	PatentIn version 3.0

PATENT NUMBER

SEQ ID No	Length	Score	DB	9;	Best Local Similarity	Matches	No. of Mismatches	No. of Indels	Gaps
1	9	100.0%	100.0%	9;	1	1	0	0	0
2	12	100.0%	100.0%	9;	1	1	0	0	0
3	9	100.0%	100.0%	9;	1	1	0	0	0
4	14	100.0%	100.0%	9;	1	1	0	0	0
5	14	100.0%	100.0%	9;	1	1	0	0	0
6	14	100.0%	100.0%	9;	1	1	0	0	0
7	14	100.0%	100.0%	9;	1	1	0	0	0
8	12	100.0%	100.0%	9;	1	1	0	0	0
9	16	100.0%	100.0%	9;	1	1	0	0	0
10	16	100.0%	100.0%	9;	1	1	0	0	0
11	16	100.0%	100.0%	9;	1	1	0	0	0
12	14	100.0%	100.0%	9;	1	1	0	0	0
13	14	100.0%	100.0%	9;	1	1	0	0	0
14	15	100.0%	100.0%	9;	1	1	0	0	0
15	15	100.0%	100.0%	9;	1	1	0	0	0

GENERAL INFORMATION
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774_0005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-208-24

Query Match	64.0%	Score 32;	DB 12;	Length 9;
Best Local Similarity	66.7%	Pred. No.	1.2e+06;	
Matches	6;	Mismatches	3;	Indels
Qy	1 CSVPLT SVC 9			
Db	1 CSPPPLTRWC 9			

RESULT 3
US-09-832-723-98

Sequence 98, Application US/09832723
; Patent No. US2002009854A1

GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar

TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
FILE REFERENCE: GC617-2

CURRENT APPLICATION NUMBER: US/09/832,723
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,259
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 117
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 98
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides screened from a phage display random library
US-09-832-723-98

Query Match	60.0%	Score 30;	DB 9;	Length 9;
Best Local Similarity	44.4%	Pred. No.	1.2e+06;	
Matches	4;	Conservative	2;	Mismatches
Qy	1 CSVPLT SVC 9			
Db	1 CCKMPTSKVC 9			

RESULT 4
US-10-303-331-98

Sequence 98, Application US/10303331
; Publication No. US20030152976A1

GENERAL INFORMATION:
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Winetzyk, Deborah S.

TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
FILE REFERENCE: GC617-3
; CURRENT APPLICATION NUMBER: US/10/303,331

GENERAL INFORMATION
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 09/832,723
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 98
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random library
US-10-303-331-98

Query Match	60.0%	Score 30;	DB 14;	Length 9;
Best Local Similarity	44.4%	Pred. No.	1.2e+06;	
Matches	4;	Conservative	2;	Mismatches
Qy	1 CSVPLT SVC 9			
Db	1 CRKMTSKVC 9			

RESULT 5
US-10-286-457-389

Sequence 389, Application US/10286457
; Publication No. US2003016004A1

GENERAL INFORMATION:
; APPLICANT: JENÓ GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
FILE REFERENCE: GPC1-P01-178

CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 389
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based on the ability to selectively bind to endothelial cells
US-10-286-457-389

Query Match	56.0%	Score 28;	DB 14;	Length 9;
Best Local Similarity	33.3%	Pred. No.	1.2e+06;	
Matches	3;	Conservative	3;	Mismatches
Qy	1 CSVPLT SVC 9			
Db	1 CDLPTSRIC 9			

RESULT 6
US-09-760-599-34

Sequence 34, Application US/09760599
; Patent No. US20010034326A1

GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
FILE REFERENCE: SC100/4-1CIP

CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-760-59-34

Query Match 52.0%; Score 26; DB 9; Length 9;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
Db 1 CALMRMSIC 9

RESULT 7

US-10-254-446A-147
; Sequence 147, Application US/1025446A
; Publication No. US2003011371A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M.
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Esther
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 147
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopan

US-10-254-446A-147

Query Match 52.0%; Score 26; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
Db 1 CKLQLTNQC 9

RESULT 10

US-10-322-266-481
; Sequence 481, Application US/10322266
; Publication No. US2004011513A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.

; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial Junctional Adhesion Molecules For Enhanced Mucosal Delivery
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 609
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct

US-10-601,953-609

RESULT 11

US-09-760-599-25
; Sequence 25, Application US/09760599
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial Junctional Adhesion Molecules For Enhanced Mucosal Delivery
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 609
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct

US-10-322-266-481

Query Match 50.0%; Score 25; DB 16; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLTSVC 9
Db 1 PVTPVC 6

RESULT 12

US-09-760-599-25
; Sequence 25, Application US/09760599

; Patent No. US20010034326A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Larson Mr., Richard S.
 ; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
 ; FILE REFERENCE: SC120074 1ICP
 ; CURRENT APPLICATION NUMBER: US/09/760,599
 ; CURRENT FILING DATE: 2001-01-17
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 25
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; US-09-760-599-25

Query Match 50.0%; Score 25; DB 9; Length 9;
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 RESULT 14
 US-10-395-032-3614
 ; Sequence 3614, Application US/10395-032
 ; Publication No. US20030229199A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Symonds, James Matthew
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; FILE REFERENCE: 100086.407C9
 ; CURRENT APPLICATION NUMBER: US/10/395, 032
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 4052
 ; SEQ ID NO: 3614
 ; SOFTWARE: PatentIn Ver. 2.0
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
 ; OTHER INFORMATION: recognition sequence
 ; US-10-395-032-3614

Query Match 50.0%; Score 25; DB 15; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1.2e+06;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 RESULT 15
 US-09-761-636A-11
 ; Sequence 11, Application US/09761636A
 ; Publication No. US2002006228A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ACHEN, Marc
 ; APPLICANT: STACKER, Steven
 ; APPLICANT: HUGHES, Richard
 ; APPLICANT: CENDRON, Angela
 ; TITLE OF INVENTION: VEGF-D/VEGFC PEPTIDOMIMETIC INHIBITOR
 ; FILE REFERENCE: 1064/4850 Achen et al
 ; CURRENT APPLICATION NUMBER: US/09/761, 636A
 ; CURRENT FILING DATE: 2001-01-18
 ; PRIOR APPLICATION NUMBER: US 60/176, 293
 ; PRIOR FILING DATE: 2000-01-18
 ; PRIORITY NUMBER: US 60/204, 590
 ; PRIOR FILING DATE: 2000-05-16
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 11

Query Match 50.0%; Score 25; DB 14; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1.2e+06;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 RESULT 13
 US-10-286-457-387
 ; Sequence 387, Application US/10286457
 ; Publication No. US2003166004A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JENO GYURIS et al.
 ; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
 ; FILE REFERENCE: GC1-P01-178
 ; CURRENT APPLICATION NUMBER: US/10/286,457
 ; CURRENT FILING DATE: 2002-11-01
 ; PRIOR APPLICATION NUMBER: 60/334822
 ; PRIOR FILING DATE: 2001-11-01
 ; NUMBER OF SEQ ID NOS: 684

i LENGTH: 7
i TYPE: PRT
i ORGANISM: Homo sapiens
US-09-761-636A-11

Query Match Score 24; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 3 vPLTS 7
 | | | |
Db 2 vPLTS 6

Search completed: September 5, 2004, 11:16:00
Job time : 36.6667 secs

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Result No.	Score	Query Match	Length	DB ID	Description
SUMMARIES					
1	26	52.0	9	4	US-09-760-599-34
2	25	50.0	9	3	US-09-258-554-199
3	25	50.0	9	3	US-09-042-107-199
4	25	50.0	9	4	US-09-187-559-3614
5	25	50.0	9	4	US-09-839-542B-3614
6	25	50.0	9	4	US-09-722-550D-199
7	25	50.0	9	4	US-09-760-599-25
8	25	50.0	9	4	US-09-483-550B-25
9	24	48.0	6	1	US-08-483-534A-21
10	24	48.0	6	3	US-08-476-134A-30
11	24	48.0	6	6	5190920-26
12	24	48.0	6	6	5506208-28
13	24	48.0	9	1	US-07-958-903A-43
14	24	48.0	9	1	US-08-462-018-43
15	24	48.0	9	1	US-08-823-345-43
16	24	48.0	9	2	US-08-598-73-49
17	24	48.0	9	3	US-08-605-430-49
18	24	48.0	9	4	US-07-963-129A-43
19	24	48.0	9	4	US-09-760-599-9
20	24	48.0	9	4	US-09-760-599-17
21	24	48.0	9	4	US-09-760-599-36
22	24	48.0	9	4	US-09-760-599-38
23	24	48.0	9	4	US-09-760-599-48
24	24	48.0	9	4	US-09-483-550B-9
25	24	48.0	9	4	US-09-483-550B-17
26	24	48.0	9	5	PCT-US92-0943A-43
27	23	46.0	8	4	US-08-475-955-67
ALIGNMENTS					
RESULT 1					
US-09-760-599-34					
; Sequence 34, Application US/09760599					
; Patent No. 6630447					
; GENERAL INFORMATION:					
; APPLICANT: Larson Mr., Richard S.					
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction					
; FILE REFERENCE: SCI2004-4-ICIP					
; CURRENT APPLICATION NUMBER: US/09-760,599					
; CURRENT FILING DATE: 2004-01-17					
; NUMBER OF SEQ ID NOS: 56					
; SOFTWARE: PatentIn Ver. 2.1					
; SEQ ID NO: 34					
; LENGTH: 9					
; TYPE: PRT					
; ORGANISM: Artificial Sequence					
; FEATURE:					
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic					
US-09-760-599-34					
RESULT 2					
US-09-258-754-199					
; Sequence 199, Application US/09258754					
; Patent No. 6174687					
; GENERAL INFORMATION:					
; APPLICANT: Ruoslahti, Erkki					
; APPLICANT: Pasqualini, Renata					
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using Membrane Dipeptidase					
; FILE REFERENCE: P-LJ-3443					
; CURRENT APPLICATION NUMBER: US/09-258,754					
; CURRENT FILING DATE: 1999-02-26					
; EARLIER APPLICATION NUMBER: US/042,107					
; EARLIER FILING DATE: 1998-03-13					
; NUMBER OF SEQ ID NOS: 452					
; SOFTWARE: PatentIn Ver. 2.0					
; SEQ ID NO: 199					
; LENGTH: 9					
; TYPE: PRT					
; ORGANISM: Artificial Sequence					

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-258-754-199

Query Match 50.0%; Score 25; DB 3; Length 9;
 Best Local Similarity 55.6%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CSVPLTSPC 9
 Db 1 CSAYTSSPC 9

RESULT 3
 US-09-042-107-199
 ; Sequence 199, Application US/09042107
 ; Patent No. 6232287
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoislahni, Erkki
 ; APPLICANT: Pasqualini, Renata
 ; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
 ; TITLE OF INVENTION: Tissues
 ; FILE REFERENCE: P-LJ 2892
 ; CURRENT APPLICATION NUMBER: US/09/042,107
 ; CURRENT FILING DATE: 1998-03-13
 ; NUMBER OF SEQ ID NOS: 436
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 199
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-042-107-199

Query Match 50.0%; Score 25; DB 3; Length 9;
 Best Local Similarity 55.6%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CSVPLTSPC 9
 Db 1 CSAYTSPC 9

RESULT 4
 US-09-187-859-3614
 ; Sequence 3614, Application US/09187859A
 ; Patent No. 6358920
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 ; FILE REFERENCE: 100086_407D1
 ; CURRENT APPLICATION NUMBER: US/09/187,859A
 ; CURRENT FILING DATE: 1998-11-06
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 3614
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
 ; OTHER INFORMATION: recognition sequence
 US-09-187-859-3614

Query Match 50.0%; Score 25; DB 4; Length 9;
 Best Local Similarity 44.4%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSPC 9
 Db 1 CSAYTSPC 9

RESULT 5
 US-09-83-9-542B-3614
 ; Sequence 3614, Application US/09839542B
 ; Patent No. 655996
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Symonds, James Matthew
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 ; FILE REFERENCE: 100086_407D1
 ; CURRENT APPLICATION NUMBER: US/09/839,542B
 ; CURRENT FILING DATE: 2001-04-20
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 3614
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
 ; OTHER INFORMATION: recognition sequence
 US-09-839-542B-3614

Query Match 50.0%; Score 25; DB 4; Length 9;
 Best Local Similarity 44.4%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSPC 9
 Db 1 CSAYTSPC 9

RESULT 6
 US-09-722-250D-199
 ; Sequence 199, Application US/09722250D
 ; Patent No. 6610651
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Eeriki
 ; APPLICANT: Pasqualini, Renata
 ; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
 ; TITLE OF INVENTION: Tissues
 ; FILE REFERENCE: P-LJ 4514
 ; CURRENT APPLICATION NUMBER: US/09/722,250D
 ; CURRENT FILING DATE: 2000-11-22
 ; PRIOR APPLICATION NUMBER: US 09/042,107
 ; PRIOR FILING DATE: 1998-03-13
 ; NUMBER OF SEQ ID NOS: 437
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 199
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-722-250D-199

Query Match 50.0%; Score 25; DB 4; Length 9;
 Best Local Similarity 55.6%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CSVPLTSPC 9
 Db 1 CSAYTSPC 9

RESULT 7
 US-09-760-599-25

; Sequence 25, Application US/09760599
 ; Patent No. 6630447
 ; GENERAL INFORMATION:
 ; APPLICANT: Larson Mr., Richard S.
 ; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
 ; FILE REFERENCE: SCI200/4-1CIP
 ; CURRENT APPLICATION NUMBER: US/09/760,599
 ; CURRENT FILING DATE: 2001-01-17
 ; NUMBER OF SEQ ID NOS: 56
 ; SEQ ID NO: 25
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 us-09-760-599-25

; ZIP: 19103-2398
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,434A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/450,738
 ; FILING DATE: 25-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/185,614
 ; FILING DATE: 24-JAN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/024,436
 ; FILING DATE: 01-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/587,197
 ; FILING DATE: 24-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/483,527
 ; FILING DATE: 22-FEB-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Leary Ph.D., Kathryn
 ; REGISTRATION NUMBER: 36,317
 ; REFERENCE/DOCKET NUMBER: 9598-3T6 (9049)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 567-3020
 ; TELEFAX: (215) 567-2991
 ; TELEX: 831-94
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-483-434A-21

Query Match Score 25; DB 4; Length 9;
 Best Local Similarity 33.3%; Pred. No. 3e+05;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
 Db 1 CMLRMNSIC 9

RESULT 8
 US-09-483-550B-25

; Sequence 25, Application US/09483550B
 ; Patent No. 6639592
 ; GENERAL INFORMATION:
 ; APPLICANT: Larson Mr., Richard S.
 ; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
 ; FILE REFERENCE: SCI200/4-001
 ; CURRENT APPLICATION NUMBER: US/09/483,550B
 ; CURRENT FILING DATE: 2000-01-14
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 25
 ; LENGTH: 9
 ; TYPE: PRT
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 us-09-483-550B-25

; Query Match Score 25; DB 4; Length 9;
 Best Local Similarity 33.3%; Pred. No. 3e+05;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9
 Db 1 CMLRMNSIC 9

RESULT 10
 US-08-476-134A-30

; Sequence 30, Application US/08476134A
 ; Patent No. 6239110
 ; GENERAL INFORMATION:
 ; APPLICANT: EVAL, JACOB
 ; APPLICANT: HAMILTON, BRUCE K.
 ; APPLICANT: TUSZINSKI, GEORGE P.
 ; TITLE OF INVENTION: SYNTHETIC ANALOGS OF THROMBOSPDIN AND THERAPEUTIC USE
 ; TITLE OF INVENTION: SYNTHETIC ANALOGS OF THROMBOSPDIN AND THERAPEUTIC USE
 ; CURRENT APPLICATION NUMBER: US/08/476,134A
 ; CURRENT FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: 07/587,197
 ; PRIOR FILING DATE: 1990-09-24
 ; PRIOR APPLICATION NUMBER: 07/483,527
 ; PRIOR FILING DATE: 1990-02-22
 ; PRIOR APPLICATION NUMBER: 08/450,738
 ; PRIOR FILING DATE: 1995-05-15
 ; PRIOR APPLICATION NUMBER: 08/185,614
 ; PRIOR FILING DATE: 1994-01-24
 ; PRIOR APPLICATION NUMBER: 08/024,436

RESULT 9
 US-08-483-434A-21

; Sequence 21, Application US/08483434A
 ; Patent No. 5648461
 ; GENERAL INFORMATION:
 ; APPLICANT: EVAL, Jacob
 ; APPLICANT: HAMILTON, Bruce K.
 ; APPLICANT: TUSZINSKI, George P.
 ; TITLE OF INVENTION: Synthetic Analogs of Thrombospondin and Therapeutic Use Thereof
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PANTICH SCHWARZE JACOBS & NADEL, P.C.
 ; STREET: 1601 Market Street, 36th Flcor
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: USA

PRIOR FILING DATE: 1993-03-01
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 30
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: synthetic
 US-08-476-134A-30

Query Match Score 24; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CSV 4
 Db 1 CSV 4

RESULT 11
 510920-26
 ; Patent No. 510920
 ; APPLICANT: EYAL, JACOB;HAMILTON, BRUCE K.;TUSZYNSKI,
 ; GEORGE P.
 ; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS
 ; OF THROMBOSPONDIN FOR INHIBITING METASTASIS ACTIVITY
 ; NUMBER OF SEQUENCES: 32
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/587,197
 ; FILING DATE: 24-SEP-1990
 ; SEQ ID NO:26;
 ; LENGTH: 6
 510920-26

Query Match Score 24; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CSV 4
 Db 1 CSV 4

RESULT 12
 5506208-38
 ; Patent No. 5506208
 ; APPLICANT: EYAL, JACOB;HAMILTON, BRUCE K.;TUSZYNSKI,
 ; GEORGE P.
 ; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF
 ; THROMBOSPONDIN FOR INHIBITING ANGIOGENESIS ACTIVITY
 ; NUMBER OF SEQUENCES: 45
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/408,181
 ; FILING DATE: 22-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 131,565
 ; FILING DATE: 04-OCT-1993
 ; APPLICATION NUMBER: 895,764
 ; FILING DATE: 09-JUN-1992
 ; APPLICATION NUMBER: 587,197
 ; FILING DATE: 24-SEP-1990
 ; SEQ ID NO:28;
 ; LENGTH: 6
 5506208-38

Query Match Score 24; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CSV 4
 Db 1 CSV 4

RESULT 13
 US-07-958-903A-43
 ; Sequence 43, Application US/07958903A
 ; Patent No. 5652214
 ; GENERAL INFORMATION:
 ; APPLICANT: Lewis, Michael E.
 ; APPLICANT: Kauer, James C.
 ; APPLICANT: Smith, Kevin R.
 ; APPLICANT: Callison, Kathleen V.
 ; APPLICANT: Baldino, Frank
 ; APPLICANT: Neff, Nicola
 ; APPLICANT: Igbal, Mohamed
 ; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION AND
 ; TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTORS AND
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3 1/2" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/958,903A
 ; FILING DATE: October 7, 1992
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/361,595
 ; FILING DATE: June 5, 1989
 ; APPLICATION NUMBER: 07/524,139
 ; FILING DATE: June 5, 1990
 ; APPLICATION NUMBER: 07/869,913
 ; FILING DATE: April 15, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 02655/003004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-07-958-903A-43

Query Match Score 24; DB 1; Length 9;
 Best Local Similarity 44.4%;
 Matches 4; Conservative 0; Mismatches 5; Indels 0;
 Gaps 0;
 Qy 1 CSVPLTSVC 9
 Db 1 CCTPAKSEC 9

RESULT 14
 US-08-462-018-43
 ; Sequence 43, Application US/08462018
 ; Patent No. 5703045
 ; GENERAL INFORMATION:
 ; APPLICANT: Lewis, Michael E.

APPLICANT: Kauer, James C.
 APPLICANT: Smith, Kevin R.
 APPLICANT: Callison, Kathleen V.
 APPLICANT: Baldino, Frank
 APPLICANT: Neff, Nicola
 APPLICANT: Iqbal, Mohamed
 TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION OF INSULIN-LIKE GROWTH FACTORS AND ANALOGS
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 502 or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/462,018
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/958,903
 FILING DATE: October 7, 1992
 APPLICATION NUMBER: 07/961,595
 FILING DATE: June 5, 1992
 APPLICATION NUMBER: 07/953,139
 FILING DATE: June 5, 1992
 APPLICATION NUMBER: 07/869,913
 FILING DATE: April 15, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 3,0,162
 REFERENCE/DOCKET NUMBER: 04655/003005
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: Linear
 US-08-462,018-43

Query Match 48.0%; Score 24; DB 1; Length 9;
 Best Local Similarity 44.4%; Pred. No. 3e+05; Mismatches 0; Gaps 0;

Qy	1	CSVPLTSVC 9	1	CSVPLTSVC 9	44.4%;
Db	1	CCTPAKSEC 9	1	CCTPAKSEC 9	0;

Search completed: September 5, 2004, 11:07:05
 Job time : 13 secs

RESULT 15
 US-08-823-245-43
 Sequence 43 Application US/08833245
 Patent No. 5776897
 GENERAL INFORMATION:
 APPLICANT: Lewis, Michael
 APPLICANT: Kauer, James C.
 APPLICANT: Smith, Kevin R.
 APPLICANT: Callison, Kathleen V.
 APPLICANT: Baldino, Frank
 APPLICANT: Neff, Nicola
 APPLICANT: Iqbal, Mohamed
 TITLE OF INVENTION: TREATING DISORDERS BY

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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:14:14 ; Search time 21 Seconds

(without alignments) 32.064 Million cell updates/sec

Title: US-09-761-636A-11

Perfect score: 42 Sequence: 1 CVPLTSC 7

Scoring table: BJOSDM2 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100%

Listing First 45 summaries

Database : PIR 78;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	47	6	B22565	R-phycoerythrin al
2	15	35	7	H48394	glycoprotein compo
3	15	35	7	I65546	MHC H2-L antigen -
4	15	35	7	B24818	viciaf 57K chain
5	15	35	7	A34026	acetylcholinesterase
6	14	33	3	E60274	major protein anti
7	13	31	0	S42620	aggrecan - bovine
8	12	28	6	I67345	R-phycoerythrin be
9	12	28	6	2	MHC H2-K ^b cell su
10	12	28	6	S08606	hypothetical prote
11	11	26	2	A2039	tyrosine-melanocyt
12	11	26	2	I54357	schwannomin - mous
13	11	26	2	A60521	glycogen Phosphory
14	11	26	2	I49421	laminin B1 - weste
15	11	26	2	E61491	seed protein ws-5
16	11	26	2	I48105	dihydrofolate redu
17	11	26	2	I48086	DNA topoisomerase
18	10	23	8	F22565	R-phycoerythrin
19	10	23	8	I37263	Y protein - human
20	10	23	8	7	catch-relaxing pep
21	10	23	8	7	tryptophyllin, bas
22	10	23	8	7	mablin II chain
23	10	23	8	7	ribulose-bisphosph
24	10	23	8	7	myomodulin - Calif
25	10	23	8	7	Ig kappa chain V-I
26	10	23	8	7	hypothetical L2 pr
27	10	23	8	7	virotoxin - destro
28	9	21	4	3	R-phycoerythrin al
29	9	21	4	4	metallothionein-A

ALIGNMENTS

RESULT 1

B22565

R-phycoerythrin alpha-2 chain - red alga (*Gastrocionium coulteri*) (fragment)
C;Species: *Gastrocionium coulteri*
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1993

C;Accession: B22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; PMID:85182601; PMID:3886644
A;Accession: B22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>

Query Match 47.6%; Score 20; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 CVP 3
|||

2 CVP 4

RESULT 2

H48394

Glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: H48394
R;Matther, I.H.; Banghart, J.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A;Reference number: A48394; PMID:93250576; PMID:8485470
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 1-6 <MAT>

Query Match 35.7%; Score 15; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy

2 VPITSC 7
|||

Db

1 VELLGC 6

RESULT 3

165546
MH-C H2-L antigen - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 165546
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their
A;Reference number: 152778; MUID:86106204; PMID:3510743
A;Accession: 165546
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: GB:MI2483; NID:9199565; PID:AAA39663.1; PMID:9554234

Query Match Score 15; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VPCT 5
Db 2 VPCT 5

RESULT 4
B34818
Vicilin 57K chain - pigeon pea (fragment)
C;Species: Cajanus cajan (pigeon pea)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C;Accession: B34818
R;Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A;Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A;Reference number: A34818; MUID:90165956; PMID:2306256
A;Accession: B34818
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 1-7 <MAW>

Query Match Score 15; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TSC 7
Db 1 TTC 3

RESULT 5
A34426
acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
C;Accession: A34426
R;Gibney, G.; MacPhae-Quigley, K.; Thompson, B.; Vedick, T.; Low, M.G.; Taylor, S.S.; T
J. Biol. Chem. 263, 1140-1145, 1988
A;Title: Divergence in primary structure between the molecular forms of acetylcholinester
A;Reference number: A34026; MUID:88087239; PMID:3335534
A;Accession: A34026
A;Residues: 1-7 <GBB>
A;Molecule type: protein
C;Keywords: alternative splicing; carboxylic ester hydrolase

Query Match Score 15; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TSC 7
Db 5 TAC 7

RESULT 6
C22565
R-phycocerythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: C22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycocerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: C22565
A;Molecule type: protein
A;Residues: 1-6 <KLO>

Query Match Score 12; DB 2; Length 6;
Best Local Similarity 25.0%; Pred. No. 2.8e+05; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LTS C 7
Db :
1 MAAC 4

RESULT 9
I67345

MHC H2-K-k cell surface glycoprotein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: I67345
 R;Archibald, A.L.; Thompson, N.A.; Kvist, S.
 EMBO J. 5, 957-965, 1986

A;Title: A single nucleotide difference at the 3' end of an intron causes differential splicing
 A;Reference number: I53243; MUID:3013627
 A;Accession: I67345
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-6 <RES>
 A;Cross-references: GB:M26859; NID:9199439; PIDN:AAA39612.1; PMID:9387458
 C;Genetics:
 A;Introns: 6/1
 C;Keywords: glycoprotein

Qy	Db	PL 4
Query Match	Best Local Similarity	28.6%; Score 12; DB 2; Length 6;
Matches 2;	Conservative	Pred. No. 2.8e+05; 0; Indels 0; Gaps 0;
Qy	4 LTSC 7	
Db	1 LPDC 4	

RESULT 10
 S08605 hypothetical protein 2 estrogen receptor 5'-region - chicken
 C;Species: Gallus gallus (chicken)
 C;Accession: S08605
 R;Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Champon, P.
 EMBO J. 5, 891-897, 1986
 A;Cross-references: EMBL:X03805; NID:963378; PIDN:CAA27432.1; PMID:9584490
 C;Superfamily: unassigned leader peptides

Qy	Db	PL 4
Query Match	Best Local Similarity	28.6%; Score 12; DB 2; Length 7;
Matches 2;	Conservative	Pred. No. 2.8e+05; 0; Indels 0; Gaps 0;
Qy	4 LTSC 7	
Db	3 LAHC 6	

RESULT 11
 A32339 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Accession: A32339
 R;Horvath, A.; Kastin, A.J.
 J. Biol. Chem. 264, 2175-2179, 1989

A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor
 A;Reference number: A32339; MUID:89123285; PMID:25633371
 A;Accession: A32339
 A;Molecule type: protein
 A;Residues: 1-4 <RES>
 A;Experimental source: brain
 C;Superfamily: unassigned animal peptides
 F;4:Modified site: amidated carboxyl end
 A;Cross-references: 1-4 <RES>

Qy	Db	PL 3
Query Match	Best Local Similarity	26.2%; Score 11; DB 2; Length 4;
Matches 2;	Conservative	Pred. No. 2.8e+05; 0; Indels 0; Gaps 0;
Qy	2 VP 3	
Db	1 VP 2	

RESULT 12
 I54357 schwannomin - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: I54357
 R;Ruyah, D.P.; Nechiporuk, T.; Pulszt, S.
 Hum. Mol. Genet. 3, 1075-1079, 1994

A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are co-expressed
 A;Reference number: I54357; MUID:95072570; PMID:7981675

Qy	Db	PL 3
Query Match	Best Local Similarity	26.2%; Score 11; DB 2; Length 4;
Matches 2;	Conservative	Pred. No. 2.8e+05; 0; Mismatches 0; Indels 0; Gaps 0;
Qy	2 VP 3	
Db	1 VP 2	

RESULT 13
 A60521 glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
 N;Alternate names: glycogen phosphorylase b
 C;Species: Liza ramada
 C;Accession: A60521
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
 Comp. Biochem. Physiol. B 95, 295-301, 1990
 A;Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
 A;Reference number: A60521; MUID:30227907; PMID:2109669
 A;Molecule type: protein
 A;Residues: 1-5 <BON>
 C;Superfamily: glucan phosphorylase
 C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
 F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experimentally confirmed

Qy	Db	PL 3
Query Match	Best Local Similarity	26.2%; Score 11; DB 2; Length 5;
Matches 2;	Conservative	Pred. No. 2.8e+05; 0; Mismatches 0; Indels 0; Gaps 0;
Qy	2 VP 3	
Db	4 VP 5	

RESULT 14
 I49421 laminin B1 - western wild mouse (fragment)
 C;Species: Mus spretus (western wild mouse)
 C;Accession: I49421
 R;Ro, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadreau, J.H.
 Mamm. Genome 5, 349-355, 1994
 A;Title: Generic mapping of 40 cDNA clones on the mouse genome by PCR
 A;Reference number: I49421
 A;Accession: I49421
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA

Qy	Db	PL 3
Query Match	Best Local Similarity	26.2%; Score 11; DB 2; Length 4;
Matches 2;	Conservative	Pred. No. 2.8e+05; 0; Indels 0; Gaps 0;
Qy	2 VP 3	
Db	4 VP 5	

A;Residues: 1-6 <RES>
A;Cross-references: EMBL:U05736; NID:g497073; PID:AAB60477.1; PID:g642829

Query Match 26.2%; Score 11; DB 2; Length 6;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TSC 7
Db ::|
Dc 3 SRC 5

RESULT 15
E61491
seed protein ws-5 - winged bean (fragment)
C.Species: Psophocarpus tetragonolobus (winged bean)
C.Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C.Accession: E61491
R.Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A.Title: Microsequence analysis of winged bean seed proteins electroblotted from two-dim
A.Reference number: A61491; MUID:89351606; PMID:2765119
A.Accession: E61491
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-7 <HIR>
C.Keywords: glycoprotein; seed

Query Match 26.2%; Score 11; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 VP 3
Db ::|
Dc 3 VP 4

Search completed: September 5, 2004, 11:19:01
Job time : 22 secs

Scoring table:	BLOSUM62	Gapop:	10.0	Gapext:	0.5	ALIGNMENTS					
Searched:	141681 seqs., 52070155 residues	Total number of hits satisfying chosen parameters:	88	Pred.	No.	Score	Query Match	Length	DB ID	Description	SEQUENCE.
Minimum DB seq length:	0	Post-processing:	Minimum Match 0%	Maximum Match 100%	Database :	SwissProt_42:*	Listing first 45 summaries			P82096 litoria rub	RESULT 1
Maximum DB seq length:	7									P23210 herpes simp	EI01_LITRU
										P42984 leptinocars	ID_B101_LITRU
										P83455 pachymedusa	STANDARD;
										P104220 mytilus edu	PRT;
										P82065 litoria rub	AC_P82096
										P82099 litoria rub	DT_28-FEB-2003
										P213799 litoria rub	DT_28-FEB-2003
										P13736 mytilus edu	(Rel. 41, Created)
										P13737 mytilus edu	DE_Electrin 1.
										P58803 conus imper	OS_Litoria rubella (Desert tree frog)
										P13071 citrobacter	OC_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
										P01373 periplaneta	OC_Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
										P36414 pseudomonas	OC_Alphaherpesvirinae; Simplexvirus.
										P11942 enterococcus	NCBI_TaxID=10306;
										P01151 pinus pinas	[1]
										P19916 pseudomonas	SEQUENCE FROM N.A.
										P36515 saccharomyces	RX_MEDLINE=91101287; PubMed=1846198;
										P01888 homo sapiens	Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B., Silverstein S., Wagner E.K.; RT_Analysis of the herpes simplex virus type 1 promoter controlling the
										P30415 bothrops in	RT
										P82100 litoria rub	DT_01-NOV-1991 (Rel. 20, Last sequence update)
										P81864 pardachirrus	DT_01-NOV-1991 (Rel. 20, Last sequence update)
										P19941 acheta dome	DT_15-MAR-2004 (Rel. 43, Last annotation update)
										P42995 leptinotarsa	DB_Capsid assembly and DNA maturation protein (Virion protein UL38).
										P41495 sarcophaga	OS_Herpes simplex virus (type 1 / strain KOS).
										P81866 carcinis ma	OC_Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
										P81867 carcinis ma	OC_Alphaherpesvirinae; Simplexvirus.
										P18108 carcinis ma	NCBI_TaxID=10306;
										P20104 enterococcus	[1]
										P16701 alcaligenes	SEQUENCE FROM N.A.
										P82101 litoria rub	RX_MEDLINE=91101287; PubMed=1846198;
										P41871 helisoma tr	Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B., Silverstein S., Wagner E.K.; RT_Analysis of the herpes simplex virus type 1 promoter controlling the
										P41875 panagrellus	RT

RT expression of UL38, a true late gene involved in capsid assembly.";
 RL J. Virol. 65:769-786(1991).
 CC -!- FUNCTION; COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
 CC EMBEDDED; BINDS DNA.
 CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).

CC DR ENB1; NS7646; AA45830; 1; -;
 KW Capsid assembly; Coat protein; DNA-binding.
 PT PRT; 6 AA; 6 MW; 67376451A336F000 CRC64;
 SQ SEQUENCE 6 AA; 703 MW;

Query Match Score 11; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PL 4
 Db 5 PL 6

RESULT 3
 ID MNP1_LEPDE STANDARD PRT; 7 AA.
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Myc peptide 1 (Lcd-MNP1).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phyoaphaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RX MEDLINE=538043; PubMed=7651886;
 RA Spitaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
 RA Grauwels L., van Leuven F., de Loof A.;
 RT "Identification, characterization, and immunological localization of
 RT a novel myotropic neuropeptide in the Colorado potato beetle,
 RT Leptinotarsa decemlineata";
 RL Peptides 16:365-374(1995).
 CC -!- FUNCTION: Myotropic peptide. Stimulates the contractions of the
 CC oviduct.
 KW Neuropептиde; Amidation.
 PT MOD RES 7 AMIDATION.
 SQ SEQUENCE 7 AA; 705 MW;

Query Match Score 11; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PL 4
 Db 5 PL 6

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tryptophyllin-1 (Pdt-1).
 OS Pachymedusa dacnicolor (Giant mexican leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyidae;
 OC Phyllomedusae; Pachymedusa.
 OX NCBI_TaxID=75988;

RN RN SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
 RP PRO-7.
 RC TISSUE-Skin secretion; Chen T. B., Or D.F., Shaw C.;
 RA "Pachymedusa dacnicolor tryptophyllin-1 (Pdt-1); structural
 RT characterization, pharmacological activity and cloning of precursor
 RT CDNA".
 RL Submitted (SEP-2002) to Swiss-Prot.
 CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
 smooth muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=109.2; METHOD=MALDI.
 DR GO:0005516; C:extracellular; NAS.
 DR GO:0045986; P:negative regulation of smooth muscle contraction.
 KW Antarctic defense peptide; Amidation; Hydroxylation.
 FT MOD RES 3 HYDROXYLATION.
 FT MOD RES 7 AMIDATION.
 SQ SEQUENCE 7 AA; 794 MW; 772237DC776350 CRC64;

Query Match Score 11; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
 Db 6 VP 7

RESULT 5
 CARP MYTED STANDARD PRT; 7 AA.
 ID CARP_MYTED
 AC P10420;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-MAR-199 (Rel. 10, Last annotation update)
 DE Catch-relaxing Peptide (CARP).
 OS Mytilus edulis (Blue mussel).
 OC Myeekyo; Metazoa; Molusca; Bivalvia; Pteriomorphia; Mytiloida;
 OC Mytilidae; Mytilidae; Mytilus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=98052022; PubMed=3676797;
 RA Hirata T., Kubota I., Kawahara A., Shimamoto N.,
 RA Munehka Y.;
 RT "Catch-relaxing Peptide isolated from Mytilus pedal ganglia.";
 RL Brain Res. 422:374-376(1987).
 CC -!- FUNCTION: This peptide exhibits both potentiating (contraction)
 CC and inhibitory (relaxation) effects on the anterior byssus
 retractor muscle.
 DR PIR; A29342; BCMUCR.
 KW Hormone; Amidation.
 FT MOD RES 7 AMIDATION.
 SQ SEQUENCE 7 AA; 831 MW; 673407687669DB0 CRC64;

Query Match Score 10; DB 1; Length 7;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPL 4
 Db 2 MPM 4

RESULT 4
 ID TPPY_PACDA STANDARD PRT; 7 AA.
 AC P83455;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

RESULT 6
 TY51_LITRU STANDARD; PRT; 7 AA.
 ID TY51_LITRU
 AC P82065;
 DT 28-FEB-2003 (Rel. 41; Created)
 DT 28-FEB-2003 (Rel. 41; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Tryptophyllin 5.1.
 OS Litoria rubella (Desert tree frog).
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodytinae; Litoria.
 NX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Skin secretion.
 RA Steinborner S.T.; Wabnitz P.A.; Waugh R.J.; Bowie J.H.; Gao C.,
 RT Tyler M.J.; Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT of evolutionary trends of amphibians.";
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study
 RL CC 4.9:955-963(1996).
 CC -!- FUNCTION: May act as a neuromodulator or neurotransmitter.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=96.5; METHOD=FAB.
 KW Amphibian defense peptide; Amidation; Neuropeptide;
 KW Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match Score 10; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 2 VP 3
 :|:
 Db 2 IP 3

RESULT 7
 E103_LITRU STANDARD; PRT; 5 AA.
 ID E103_LITRU
 AC P82059;
 DT 28-FEB-2003 (Rel. 41; Created)
 DT 28-FEB-2003 (Rel. 41; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DB Electric 3.
 OS Litoria rubella (Desert tree frog).
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodytinae; Litoria.
 NX NCBI_TaxID=104895;
 RN SEQUENCE.
 RC TISSUE-Skin secretion;
 RA Wabnitz P.A.; Bowie J.H.; Tyler M.J.; Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RT Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: Skin. Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense Peptide; Amidation.
 FT MOD RES 5 5 AMIDATION
 SQ SEQUENCE 5 AA; 630 MW; 688761F2C9A00000 CRC64;

Query Match Score 9; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 3 PL 4
 |:

RESULT 8
 CIP1_MYTED STANDARD; PRT; 6 AA.
 ID CIP1_MYTED
 AC P13736;
 DT 01-JAN-1990 (Rel. 13; Created)
 DT 01-JAN-1990 (Rel. 13; Last sequence update)
 DT 15-DEC-1998 (Rel. 37; Last annotation update)
 DE Contraction-inhibiting peptide I (MIP I).
 OS Mytilus edulis (Blue mussel).
 OC Bivalvia; Mollusca; Mytilidae; Mytilus.
 OC Mytiloidea; Mytilidae; Mytilus.
 OC Mytiloidea; Mytilidae; Mytilus.
 NX NCBI_TaxID=6550;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=1377776;
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=1377776;
 RA Hirata T., Kubota I.; Iwasawa N.; Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides.";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -!- FUNCTION: Inhibitory action on contractions in several molluscan
 CC muscles.
 CC -!- SIMILARITY: TO MIP II.
 CC DR PIR: A27696; B27696.
 KW Hormone; Amidation.
 FT MOD RES 6 AMIDATION.
 SQ SEQUENCE 6 AA; 637 MW; 72C9C6875B81000 CRC64;

Query Match Score 9; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 3 PL 4
 |:

RESULT 9
 CIP2_MYTED STANDARD; PRT; 6 AA.
 ID CIP2_MYTED
 AC P13737;
 DT 01-JAN-1990 (Rel. 13; Created)
 DT 01-JAN-1990 (Rel. 13; Last sequence update)
 DT 15-DEC-1998 (Rel. 37; Last annotation update)
 DE Contraction-inhibiting peptide II (MIP II).
 OS Mytilus edulis (Blue mussel).
 OC Bivalvia; Mollusca; Bivalvia; Mytiloidea; Mytilus.
 OC Mytiloidea; Mytilidae; Mytilus.
 OC Mytiloidea; Mytilidae; Mytilus.
 NX NCBI_TaxID=6550;
 RN SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=1377776;
 RA Hirata T., Kubota I.; Iwasawa N.; Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides.";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -!- FUNCTION: Inhibitory action on contractions in several molluscan
 CC muscles.
 CC -!- SIMILARITY: TO MIP I.
 CC DR PIR: B27696; B27696.
 KW Hormone; Amidation.
 FT MOD RES 6 AMIDATION.
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match Score 9; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 3 PL 4
 |:

[4]

RN	SEQUENCE;	Qy	2 VP 3
RP	SPECIES;C.maenas;	Db	:
RC	Medline:8622789; PubMed=872661;		5 LP 6
RX	"Stangier J., Dirksen H., Keller R., RT "Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, <i>Carcinus maenas</i> ."; RL Peptides 7:67-72(1986).		
CC	-!- FUNCTION: Stimulates cardiac output and hindgut motility modulates visceral and skeletal muscle in many arthropods.		
CC	-!- TISSUE SPECIFICITY: Found in the lateral white neurons and in the crab pericardial organs.		
DR	PIR; A01644; HOROHA.		
DR	PIR; A60411; A60411.		
KW	Neuropeptide.		
SQ	SEQUENCE 5 AA; 649 MW; 71B7673BA44600000 CRC64;		

Query Match Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	2 VP 3	Db	:
	3 LP 4		

RESULT 14

ID	CIA_ENTFA	STANDARD;	PRT;
AC	PL1932;		7 AA.
DT	01-OCT-1989 (Rel. 12, Created)		
DT	01-OCT-1989 (Rel. 12, Last sequence update)		
DT	01-FEB-1991 (Rel. 17, Last annotation update)		
DE	Sex pheromone CAM373 (Clumping-inducing agent) (CIA).		
OS	Enterococcus faecalis (Streptococcus faecalis) (Enterococcaceae, Enterococcus,		
OC	Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.		
OX	NCBI_TaxID:1351;		

Query Match Score 8; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	2 VP 3	Db	:
	3 LP 4		

RESULT 15

ID	TRPI_PSEPU	STANDARD;	PRT;
AC	P36474;		6 AA.
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	HTH-type transcriptional regulator trpi (TrpBA operon transcriptional activator) (Fragment).		
GN	TRPI.		
OS	Pseudomonas putida.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		
OC	Pseudomonadaceae; Pseudomonas.		
OX	NCBI_TaxID=303;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=PPE1 CLS;		
RX	Medline:83335826; PubMed=2503057;		
RA	Eberly L., Crawford I.P.;		
RT	"DNA Sequence of the tryptophan synthase genes of Pseudomonas putida." Biochimie 71:521-531(1989).		
RL			
CC	-!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE TRPBA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.		
CC	-!- SIMILARITY: Contains 1 HTH LYR-type DNA-binding domain.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	EMBL; X1:3299; CAA31660.1;		
CC	DR InterPro; IPR00841; FTH LysR.		
CC	DR PROSITE; PS50331; FTH LYSR; PARTIAL.		
CC	KW TRYptophan biosynthesis; Transcription regulation; Activator;		
CC	KW DNA-binding.		
FT	NON TER 6 6		
SQ	SEQUENCE 6 AA; 683 MW; 71672AA1EDD6F000 CRC64;		

Query Match Score 8; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	2 VP 3	Db	:
	3 LP 4		

RESULT 16

ID	UN06_PINPS	STANDARD;	PRT;
AC	P81675;		7 AA.
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Unknown protein from 2D-page of needles (N141) (Fragment).		
OS	Pinus pinaster (Maritime pine).		
CC	-!- SIMILARITY: Variodiplante; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.		
CC	"Separation and characterization of needle and xylem maritime pine proteins." Electrophoresis 20:1098-1108(1999).		
CC	-!- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown protein is: 6.6, its MW is: 25 kDa.		
FT	NON TER 1 1		
FT	NON TER 7 7		
SQ	SEQUENCE 7 AA; 823 MW; 69D7672446B5740 CRC64;		

Query Match Score 8; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	2 VP 3	Db	:
	3 LP 4		

Sun Sep 5 11:41:03 2004

us-09-761-636a-11.closed.rsp

Page 6

QY 2 VP 3
Db :|
5 LP 6

Search completed: September 5, 2004, 11:17:30
Job time : 17 secs

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OM protein - protein search, using SW model

Run on: September 5, 2004, 11:13:09 (without alignments)

38.748 Million cell updates/sec

Title: US-09-761-636A-11

Perfect score: 42

Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315516202 residues

Total number of hits satisfying chosen parameters: 74

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SPTRMBL25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archeap:*

ALIGNMENTS

RESULT 1

Q66113 ID Q66113 PRELIMINARY; PRT; 7 AA.

AC Q66113; DT 01-NOV-1996 (TREMBL; 01, Created)

DT 01-NOV-1996 (TREMBL; 01, Last sequence update)

DT 01-DEC-2001 (TREMBL; 19, Last annotation update)

DE C-terminus of the viral replicase (Fragment).

OS Cherry leaf roll virus.

Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;

OC Nepovirus,

OX NCBI_TaxID=12615;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Walnut;

RA Boria M.

RL Thesis (1992), Biología Molecular y Virología Vegetal, CIT-INIA.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB	ID	Description
<hr/>						
1	17	40.5	7	12	Q66113	066113 cherry leaf
2	15	35.7	7	13	042564	042564 fugu rubrip
3	12	28.6	5	13	P83308	P83308 gallus galli
4	12	28.6	7	12	Q67113	Q67113 influenzae
5	11	26.2	7	4	Q8NNHH7	Q8NNHH7 homo sapien
6	11	26.2	7	8	Q8MFY6	Q8MFY6 taraxacum (
7	11	26.2	7	10	P93233	P93233 lycopersico
8	10	23.8	7	2	P70804	P70804 azotobacter
9	10	23.8	7	2	P7081	P72081 nocardia la
10	10	23.8	7	2	Q8GL12	Q8GL12 borrelia bu
11	10	23.8	7	10	Q9CB5B3	Q9CB5B3 arabiopsis
12	10	23.8	7	15	Q7624	Q7624 rous sarcom
13	9	21.4	6	5	P83569	P83569 sepiia offic
14	9	21.4	7	2	Q54248	Q54248 actinobacil
15	9	21.4	7	2	Q54248	Q54248 streptomyce
16	9	21.4	7	11	Q55184	Q55184 rattus norv

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB	ID	Description
<hr/>						
1	17	40.5	7	12	Q66113	066113 cherry leaf
2	15	35.7	7	13	042564	042564 fugu rubrip
3	12	28.6	5	13	P83308	P83308 gallus galli
4	12	28.6	7	12	Q67113	Q67113 influenzae
5	11	26.2	7	4	Q8NNHH7	Q8NNHH7 homo sapien
6	11	26.2	7	8	Q8MFY6	Q8MFY6 taraxacum (
7	11	26.2	7	10	P93233	P93233 lycopersico
8	10	23.8	7	2	P70804	P70804 azotobacter
9	10	23.8	7	2	P7081	P72081 nocardia la
10	10	23.8	7	2	Q8GL12	Q8GL12 borrelia bu
11	10	23.8	7	10	Q9CB5B3	Q9CB5B3 arabiopsis
12	10	23.8	7	15	Q7624	Q7624 rous sarcom
13	9	21.4	6	5	P83569	P83569 sepiia offic
14	9	21.4	7	2	Q54248	Q54248 actinobacil
15	9	21.4	7	2	Q54248	Q54248 streptomyce
16	9	21.4	7	11	Q55184	Q55184 rattus norv

Query Match 40.5% Score 17; DB 12; Length 7;

Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QV 1 CVP 3

Db 4 CLP 6

RESULT 2
O42564 PRELIMINARY; PRT; 7 AA.
ID O42564
AC 042564
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JUN-2003 (TREMBLrel. 05, Last sequence update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
AC Acanthomorpha; Acanthopterygii; Teleostei; Butelostomi; Neoteleostei; Tetraodontiformes;
CC Tetradontoidea; Tetraodontidae; Takifugu.
OC NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MBDLINER=9742476; PubMed=9295352;
RA Plummer N.W.; McIntrye M.W.; Meissner M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
two-domain protein in fetal brain and non-neuronal cells";
RU J. Biol. Chem. 272:24008-24015(1997).
DR EMBL: U97673; AAB80916; -
DR GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON_TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C3772A0 CRC64;
Query Match 35.7%; Score 15; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VPL 4
DB 1 VPL 3

RESULT 4
Q67113 PRELIMINARY; PRT; 7 AA.
ID Q67113
AC Q67113
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) CDNA, 3' end
DE (Fragment).
OS Influenzavir. A.
OC ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001892; PubMed=7407922;
RA Dhar R.; Chanock R.M.; Lai C.-J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
viral mRNA deduced from cloned complete genomic sequences.";
RU Cell 21:495-500(1980).
DR M25045; AAC4320; 1; -
FT NON_TER 1
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;
Query Match 28.6%; Score 12; DB 12; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
QBNNH7 PRELIMINARY; PRT; 7 AA.
ID QBNNH7
AC QBNNH7
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE Mini-cistron.
GN NHEJ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MaLakooti J.; Ramaswamy K.;
RT "Molecular cloning and characterization of the human Na+/H+ exchanger
NHE-3 gene promoter region";
RC Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL DR EMBL: AF282824; AAC53436; 1; -
SQ SEQUENCE 7 AA; 842 MW; 74072DC772D406F0 CRC64;
Query Match 26.2%; Score 11; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VP 3
DB 3 VP 4

RESULT 6
Q8MFY6 PRELIMINARY; PRT; 7 AA.
ID Q8MFY6
AC Q8MFY6
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Fmrfamide-like neuropeptide (LPRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN 1
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX Published=6137771;
RA Dockray G.J.; Reeve J.R. Jr.; Shirely J.; Gayton R.J.; Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
antibodies to FMRFamide.";
RL Nature 305:328-330(1983).
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO:00007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 5 AA; 645 MW; AMIDATION.
SQ SEQUENCE 5 AA; 645 MW; 69D407367400000 CRC64;
Query Match 28.6%; Score 12; DB 13; Length 5;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 VPL 4
DB 1 VPL 3

DE	PsBA (Fragment).	DT	01-FEB-1997 (TREMBLrel. 02; Created)
GN	PSBA.	DT	01-FEB-1997 (TREMBLrel. 02; Last sequence update)
OS	Taraxacum (sect. Dioszegia) sp. 4310Hnew.	DT	01-DEC-2001 (TREMBLrel. 19; Last annotation update)
OG	Chloroplast.	DE	AlgT protein (Fragment).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	GN	AUGT.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;	OS	Azotobacter vinelandii.	
Campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	
Taraxacum.	OC	Pseudomonadaceae; Azotobacter.	
NCBI_TaxID=154248;	OX	NCBI_TaxID=354;	
RN [1]	RN [1]	RN [1]	RN [1]
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC TISSUE-Leaf;	RC STRAIN-E;	RC MEDLINE=96427318; PubMed=8830682;	RC
RA Mes T.H.M.;	RA Rehm B.H.A., Ertesvag H., Valli S.;	RA RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is part of an alg gene cluster physically organized in a manner similar to that in <i>Pseudomonas aeruginosa</i> .";	RA
RT "Reconstruction of the evolution of trnP pseudogenes.";	RT RT J. Bacteriol. 178:5884-5889(1996).	RT RL DR EMBL; X87973; CAA61230.1; -.	RT
RL Submitted (NOV-2000) to the EMBL/Genbank/DDBJ databases.	DR	FT NON TER FT NON TER	FT
DR BMBL; AY015077; AAK21591.1;	GO; GO:0009307; C:chloroplast; IEA.	SQ SEQUENCE 7 AA; 675 MW; 687451B5A76DDB70 CRC64;	SQ SEQUENCE 7 AA; 684 MW; 71B5A5A2D1AED0 CRC64;
KW Chloroplast.	FT NON TER	Query Match Best Local Similarity 50.0%; Pred. No. 1e+06; Length 7; Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Query Match Best Local Similarity 23.8%; Pred. No. 1e+06; Length 7; Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
FT SEQUENCE 7 AA; 675 MW;	Db 3 PLTS 6	Qy 1 CVDPLS 6	Qy 1 CVDPLS 6
Db 3 PSTN 6	Db 1 CTVSSS 6	Db 1 CTVSSS 6	Db 1 CTVSSS 6
RESULT 7	P93233 PRELIMINARY; PRT; 7 AA.	P72081 PRELIMINARY; PRT; 7 AA.	RESULT 9
ID P93233	AC P93233;	ID P72081	AC P72081;
AC P93233;	DT 01-MAY-1997 (TREMBLrel. 03; Created)	AC AC	DT DT
DT 01-MAY-1997 (TREMBLrel. 03; Last sequence update)	DT 01-MAY-1997 (TREMBLrel. 03; Last sequence update)	DT 01-FEB-1997 (TREMBLrel. 02; Created)	DT 01-FEB-1997 (TREMBLrel. 02; Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24; Last annotation update)	DE 1-aminoacylpropane-1-carboxylate synthase (EC 4.4.1.14)	DT 01-DEC-2001 (TREMBLrel. 19; Last annotation update)	DE 3'-methylcephem hydrolase (Fragment).
DE 1-aminoacylpropane-1-carboxylate synthase (EC 4.4.1.14)	DE (Fragment).	GN CEPP	GN Nocardia lactamdurans.
DE (Fragment).	GN Lycopersicon esculentum (Tomato).	RA Coque J., Perez-Llarena F.J., Enguita F.J., Martin J.F., Liras P.;	RA Bacteria; Actinobacteria; Actinomycetales;
GN Lycopersicon esculentum (Tomato).	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	RT RT Striromyces clavuligerus encoding a functional 3'-hydroxymethylcephem O-carbamoyltransferase for cephanyacin biosynthesis.";	OC Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;	OC Lamidae; Solanaceae; Solanaceae; Solanaceae; Solanaceae;	Gene 162:21-27(1995).	OC NCBI_TaxID=1913;
OC NCBI_TaxID=4081;	RN [1]	DR Z211682; CAA19797.1; -.	RN [1]
RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.	FT NON TER FT NON TER	FT NON TER
RX MEDLINE=971351561; PubMed=9207843;	RX MEDLINE=96009872; PubMed=7557411;	SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;	SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;
RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;	RA RA	Query Match Best Local Similarity 23.8%; Pred. No. 1e+06; Length 7; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Query Match Best Local Similarity 23.8%; Pred. No. 1e+06; Length 7; Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
RT "Differential induction of seven 1-aminoacylcopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato (Lycopersicon esculentum)." ;	RT RT	Qy 4 LTS 6	Qy 5 VTS 7
RT synthase genes by elicitor in suspension cultures of tomato (Lycopersicon esculentum)." ;	RT Striromyces clavuligerus encoding a functional 3'-hydroxymethylcephem O-carbamoyltransferase for cephanyacin biosynthesis.";	Db	Db
RT Plant Mol. Biol. 34:275-286(1997).	RL Gene 162:21-27(1995).	DR	RESULT 10
RL DR; GO:0016847; F:1-aminoacylcopropane-1-carboxylate synthase . . . IEA.	DR DR; GO:0016829; F:lyase activity; IEA.	DR Z211682; CAA19797.1; -.	Q8GL12 PRELIMINARY; PRT; 7 AA.
DR DR; GO:0016829; F:lyase activity; IEA.	DR DR; GO:0016829; F:lyase activity; IEA.	DR NON TER	Q8GL12 PRELIMINARY; PRT; 7 AA.
DR Lysine.	DR Lysine.	SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;	Q8GL12 PRELIMINARY; PRT; 7 AA.
FT NON TER 1	FT NON TER 1	Query Match Best Local Similarity 26.2%; Score 11; DB 10; Length 7; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Q8GL12 PRELIMINARY; PRT; 7 AA.
SQ SEQUENCE 7 AA; 828 MW;	SQ SEQUENCE 7 AA; 828 MW;	Qy 3 PL 4	Qy 3 PL 4
Query Match Best Local Similarity 100.0%; Pred. No. 1e+06; Length 7; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Best Local Similarity 100.0%; Pred. No. 1e+06; Length 7; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db 3 PL 4	Db 3 PL 4
Qy 3 PL 4	Qy 3 PL 4	Db 5 VTS 7	Db 5 VTS 7
Db 3 PL 4	Db 3 PL 4	RESULT 8	RESULT 8
RESULT 8	P70804 PRELIMINARY; PRT; 7 AA.	P70804 PRELIMINARY; PRT; 7 AA.	P70804 PRELIMINARY; PRT; 7 AA.
ID P70804	AC P70804,	AC P70804,	AC P70804,
DT 01-MAR-2003 (TREMBLrel. 23; Created)	DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	DT 01-MAR-2003 (TREMBLrel. 24; Last annotation update)	DT 01-JUN-2003 (TREMBLrel. 24; Last annotation update)

DE	PF-50 protein (Fragment).	OS	Rous sarcoma virus (strain Prague C).
GN	PF-50.	OC	Viruses; Retroviridae; Alpharetrovirus.
OS	Borrelia burgdorferi (Lyme disease spirochete).	NCBI_TaxID	11888;
OG	Plasmid group CP32-9.	RN	[1]
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.	SEQUENCE FROM N.A.	
OX		RX	SEQUENCE FROM N.A.
RN	[1]	MEDLINE	93010967; PubMed=1327749;
RP	SEQUENCE FROM N.A.	RA	Donne O.; Spaeth P.F.;
RC	STRAIN=NA40;	RT	"Role of the open reading frames of Rous sarcoma virus leader RNA in translation and genome packaging."
RA	Miller J.C. Miller B., Miller J.C. Comparative analyses of Borrelia burgdorferi erp genes and their cp32-9 prophages: conservation amidst diversity;"	RT	EMBO J. 11:3747-3757(1992).
RT	Submitted (AUG-2002) to the EMBL/Genbank/DDBJ databases.	RL	EMBL; X67587; CAA47862.1; -
RL	EMBL; AY142100; AAN17911.1; -	DR	776045A7687DD6F0 CRC64;
DR	Go; Go:046821; c:extrachromosomal DNA; IFA.	SQ	SEQUENCE 7 AA; 672 MW;
KW	Plasmid.	Query Match	23.8%; Score 10; DB 15; Length 7;
FT	NON TER 1	Best Local Similarity	50.0%; Pred. No. 1e+06;
SQ	SEQUENCE 7 AA; 849 MW;	Matches	1; Mismatches 0; Indels 0; Gaps 0;
QY	23.8%; Score 10; DB 2; Length 7;	QY	2 VP 3
Db	Pred. No. 1e+06; 1; Mismatches 0; Indels 0; Gaps 0;	Db	6 IP 7
	RESULT 13		
QY	1 CV 2	Q3569	PRELIMINARY; PRT; 6 AA.
Db	1 CM 2	ID	P83569
		AC	P83569;
		DT	01-JUN-2003 (TREMBLrel. 24, Created)
		DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
Q9C5B3	PRELIMINARY;	DE	Sperm attracting peptide SPSAP.
Q9C5B3	PRT; 7 AA.	OS	Sepia officinalis (Common cuttlefish)
AC	Q9C5B3; 2001 (TREMBLrel. 17, Created)	OC	Eukaryota; Metazoa; Molusca; Cephalopoda; Coleoidea; Neocoelioidea;
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	NCBI_TaxID	6610;
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	RN	[1]
DE	Hypothetical protein (Fragment).	RP	SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND AMIDATION.
DN	DID1 10A-2B.	RC	TISSUE=Egg;
OS	Arabidopsis thaliana (Mouse-ear cress); Embryophyta; Tracheophyta;	RX	PubMed=12207899;
OC	Buturophyta; Viridiplantae; Streptophytina; Rosids; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; rosids;	RA	Zatlyn C.; Marvin L.; Gagnon J.; Henry J.;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.	RT	"Fertilization in <i>Sepia officinalis</i> : the first mollusk sperm-
OX		RT	attracting peptide."
RN	[1]	RL	Biomed. Biophys. Res. Commun. 296:1186-1193 (2002).
RP	SEQUENCE FROM N.A.	CC	-1- FUNCTION: ATTRACTS SPERM INCREASING THE CHANCES OF GAMETE COLLISION.
RC	TISSUE=ROOT.	CC	-1- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE OVARIAN FOLLICLES DURING VITELLOGENESIS. ACCUMULATES IN THE OCYCLES BEFORE BEING SECRETED DURING FERTILIZATION. EXPRESSION CONTINUES IN THE EMBEDDED OCYTE.
RX	MEDLINE=21171025; PubMed=11277426;	CC	CC ACCUMULATES IN THE EGG CAPSULE AFTER FERTILIZATION.
RA	Vercauteren I.; Van Der Schueren E.; Van Montagu M.; Gheysen G.;	CC	-1- MASS SPECTROMETRY: MW=556.6; METHOD=MALDI.
RT	"Arabidopsis thaliana genes expressed in the early compatible interaction with root-knot nematodes";	KW	Amidation.
RT	RT interaction with root-knot nematodes.";	FT	MOD RES 6 AA; 597 MW; 72C8676AA0470000 CRC64;
RL	Mol. Plant Microbe Interact. 14:288-299 (2001).	SQ	SEQUENCE 6 AA; 597 MW;
DR	EMBL; AB286350; CAB71014.2; -.	Query Match	21.4%; Score 9; DB 5; Length 6;
KW	Hypothetical protein.	Best Local Similarity	50.0%; Pred. No. 1e+06;
FT	NON TER 1	Matches	1; Mismatches 0; Indels 0; Gaps 0;
SQ	SEQUENCE 7 AA; 719 MW;	QY	3 PL 4
QY	23.8%; Score 10; DB 10; Length 7;	Db	1 PR 2
Db	Pred. No. 1e+06; 1; Mismatches 1; Indels 0; Gaps 0;	RESULT 14	
	5 TSC 7	050556	PRELIMINARY; PRT; 7 AA.
	:	ID	050556
	1 SKC 3	AC	050556;
		DT	01-JUN-1998 (TREMBLrel. 06, Created)
RESULT 12		DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)
Q97624	PRELIMINARY;	DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
TD	PRT; 7 AA.	DE	GLYA (Fragment).
AC	Q97624; 01 (TREMBLrel. 01, Created)	GN	GLYA.
Q97624	01 (TREMBLrel. 01, Last sequence update)	OS	Actinobacillus actinomycetemcomitans (Haemophilus UORF1).

OS actinomycetemcomitans;
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Actinomycetemcomitans;
 OX NCBI_TAXID=714;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33384;

RX MEDLINE=96355846; PubMed=8751884;

RA Kolodrubetz D., spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,

RA Kraig E.;

RT "cis Elements and trans factors are both important in strain-specific

regulation of the leukotoxin gene in *Actinobacillus* "

RT actinomycetemcomitans";

RL Infect. Immun. 64:3451-3460(1996).

DR EMBL; U51862; AAB88721.1; -.

FT NON TER 1 1

SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 21.4%; Score 9; DB 2; Length 7;

Best Local Similarity 33.3%; Pred. No. 1e+06; Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPL 4

Db 3 LPV 5

RESULT 15

Q54248 ID Q54248 PRELIMINARY; PRT; 7 AA.

AC Q54248;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE RPL0 protein (Fragment).

GN RPL0.

OS Streptomyces griseus.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomyceae; Streptomyctaceae; Streptomyces.

OX NCBI_TAXID=1911;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=N2-3-11;

RX MEDLINE=20011291; PubMed=10542330;

RA Poehling S., Pieperberg W., Wehmeier U.F.;

RT "Analysis and regulation of the sec Y gene from *Streptomyces griseus*

N2-3-11 and interaction of the SecY protein with the SecA protein.";

RL Biochim. Biophys. Acta 1447:298-302(1999).

DR EMBL; X95915; CAA65160.1; -.

FT NON TER 1 1

SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match 21.4%; Score 9; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VPLT 5

Db 1 VTVT 4

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine 2 residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excess vascular tone related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

Qy	Sequence 7 AA;	Score 42;	DB 4;	Length 7;
	Query Match	100.0%		
	Best Local Similarity	100.0%	Pred. No.	1.4×10^6
	Matches 7;	Conservative	Mismatches	0;
			Indels	0;
			Caps	0;
Db	CVPLTSC	7		
	CVPLTSC	7		

RESULT 2
 AAW13421 ID AAW13421 standard; peptide; 7 AA.
 XX AC AAW13421;
 XX DT 15-JAN-1998 (first entry)
 XX DE Kidney homing peptide.
 XX KW Kidney homing peptide; in vivo panning; screening; phage display;
 XX KW drug delivery.

XX PS Claim 16; Page 68; 75pp; English.
XX This synthetic peptide is a claimed example of a kidney-homing peptide
CC that was identified using a novel method for obtaining molecules that
CC home to a selected organ or tissue. This *in vivo* panning method typically
CC

involves administering a phage display library to a subject, and identifying expressed peptides which home to the desired organ or tissue, e.g. brain, kidney, angiogenic vascular tissue or tumour tissue. The isolated peptides (see AAW13412-52, AAW11181-16) can be used to target e.g. drugs, toxins or labels to the selected organ/tissue (claimed) or to identify and/or isolate target molecules (claimed). The Peptides can be directly identified in vivo, as compared to prior art in vitro screening methods, which require further examination to see if they maintain specificity in vivo

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Q Sequence 7 AA;
Q Query Match 73.8%; Score 31; DB 2; Length 7;
Q Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Q Matches 4; Conservative 2; Mismatches 1; Indels 0;
Q Gaps 0

QY 1 CYPBLTSC 7
Db 1 CLPVAASC 7

RESULT 2
ARAB12007

```

AAB12007 ID AAB12007 standard; peptide; 7 AA.
 XX
 AAB12007;
 XX
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Kidney homing peptide # 1.
 XX
 KW Kidney; homing peptide; organ targeting; tissue targeting; mouse; cyclic
 XX

DR WPI; 2000-410050/35.
 XX Identifying and recovering organ homing molecules or peptides by in vivo panning comprises administering a library of diverse peptides linked to a tag which facilitates recovery of these peptides.

XX Example 2; Col 18; 20pp; English.

XX The present sequence is a mouse kidney homing peptide. This sequence was identified by using in vivo panning to screen a library of potential organ homing molecules. The present sequence can be used to direct a moiety to a kidney tissue, by linking the moiety to the present sequence. Examples of potential moieties are drugs, toxins or a detectable label.

XX Sequence 7 AA:
 SQ

Ov	1	CVPILTSC	7
Query Matches	4	Conservative	
Best Local Similarity	57.1%		
Match Score	31;	DB 3;	Length 7;
Pred.	No.	1.4e+06	
Mismatches	2;	Mismatches	1;
Indels			0;
Gaps			

Db	1 : :	1 CLPVASC 7	
RESULT 4			
AAU1813	standard; peptide; 7 AA.		
ID	AAE11813		
XX			
AC	AAE11813;		
XX			Kidney homing peptide #1 useful for delivery of target molecules.
DT	11-SEP-2003 (revised)		
DT	18-DEC-2001 (first entry)		
XX			Organ targeting; tissue targeting; cancer; tumour homing molecule; delivery of target molecule; kidney homing peptide.
DE			
XX			Synthetic.
OS			
XX			XX DE XX
PN	US6305365-B1.		KW KW
XX			XX
PD	23-OCT-2001.		PP 08-JAN-1999;
XX			XX 99US-002227906.
PR	11-SEP-1995;		PR 10-MAR-1997;
PT	95US-00526710.		PR 23-JUN-1997;
XX			XX 97US-0081273.
PS	PA (BURN-) BURNHAM INST.		XX 97US-00862855.
XX			PA PA
PI	Ruosahti E, Pasqualini R;		XX PI
XX			XX DR
DR	2002-040196/05.		XX WPI; 2002-040196/05.
XX			
PP	08-JAN-1999;	99US-00226985.	PT Recovering molecules that home to an organ or tissue, useful for identifying molecules that home to a specific organ or tissue, e.g. PT identifying a tumor homing molecule to identify the presence of cancer, e.g. PT by in vivo panning of a library.
XX			XX Example 2; Col 18; 21pp; English.
PR	11-SEP-1995;	95US-00526710.	CC The present invention relates to a method of recovering molecules that home to a selected organ or tissue. The method comprises administering to the subject the library of diverse molecules, collecting a sample of the selected organ or tissue (e.g., brain or kidney), and recovering from the sample several molecules that home to the selected organ or tissue. The method is useful for identifying molecules, particularly useful for screening large number of molecules (e.g.: peptides), that home to a specific moiety. The identified molecule is useful for e.g. raising an antibody specific for a target molecule, targeting a desired moiety (e.g., drug, toxin or detectable label) to the selected organ. Specifically, the method is useful for identifying the presence of cancer in a subject by linking an appropriate moiety to a tumour homing molecule. The present method provides a direct means for identifying molecules that specifically home to a selected organ and, therefore provides a significant advantage over previous methods, which require that a molecule identified using an in vitro screening method subsequently be examined to determine if it maintains its specificity in vivo. AAU10724-AAU10738 represent kidney homing peptides described in the present invention
PR	10-MAR-1997;	97US-0081273.	CC SQ Sequence 7 AA;
PR	23-JUN-1997;	97US-00862855.	CC Query Match 73.8%; Score 31; DB 5; Length 7;
XX			CC Best Local Similarity 57.1%; Pred. No. 1.4e+06; Mismatches 2; Indels 0; Gaps 0;
PA	(BURN-) BURNHAM INST.		XX AC ABUS9533;
XX			XX AC ABUS9533;
PI	Ruosahti E, Pasqualini R;		XX AC ABUS9533;
XX			XX AC ABUS9533;
DR	2001-610691/70.		XX AC ABUS9533;
XX			XX AC ABUS9533;
PT	Enriched library fraction comprising molecules recovered by in vivo panning that selectively home to a selected organ or tissue useful for treating disease or in diagnostic methods.		XX AC ABUS9533;
PT	Example 2; Col 18; 21pp; English.		XX AC ABUS9533;
XX			XX AC ABUS9533;
PS	Enriched library fraction containing molecules that selectively home to a selected organ or tissue such as brain, kidney or tumour recovered by in vivo panning. The invention generally relates to the field of molecular medicine, drug delivery and to a method of in vivo panning for identifying a molecule that homes to a specific organ. The molecules, e.g., peptides, Peptidomimetics, proteins and fragments of proteins contained in an enriched library fraction may be administered to a subject as part of a pharmaceutical composition to treat disease or in diagnostic methods. The present sequence is a peptide from bacteriophage targeted to kidney. (Updated on 11-SEP-2003 to standardise OS field)		XX AC ABUS9533;
XX			XX AC ABUS9533;
PS	Sequence 7 AA;		XX AC ABUS9533;
XX			XX AC ABUS9533;
QY	1 CVPITSC 7		XX AC ABUS9533;
Db	1 CLPVASC 7		XX AC ABUS9533;
RESULT 5			
AAU10724	standard; peptide; 7 AA.		
ID	AAU10724		
XX			XX DT 22-APR-2003 (first entry)
AC	AAU10724;		XX DE Kidney receptor targeting peptide #1.
XX			XX DT Targeting ligand; bioactive agent; polymer matrix; cancer; cytosatic;
DT	12-MAR-2002 (first entry)		XX KW

cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
tumour; cationic cancer-targeting peptide.

Synthetic.

US2002041898-A1.
 PN XX
 XX XX
 PD XX
 11-APR-2002.
 XX XX
 PP XX
 25-JUL-2001; 2001US-00912609.
 PR XX
 05-JAN-2000; 2000US-00478124.
 PR XX
 31-OCT-2000; 2000US-00703474.
 PA XX
 (UNGE/) UNGER B. C.
 (MATS/) MATSUNAGA T. O.
 PA PA
 (RAMA/) RAMASWAMI V.
 PA PA
 (ROMA/) ROMANOWSKI M. J.
 XX PI
 Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
 XX DR
 WPI; 2003-208921/20.

Targeted delivery system comprising a bioactive agent homogeneously dispersed in a targeted matrix is especially useful in cancer therapy.

Claim 25; Page 38; 46pp; English.

The invention relates to a composition comprising a bioactive agent homogeneously dispersed in a targeted matrix (polymer and targeting ligand). Also included are a targeted matrix for use as a delivery vehicle comprising a polymer associated with a targeting ligand, enhancing the bioavailability of an agent comprising administration of the composition and treating cancer comprising administration of the novel composition. The method is useful for targeted delivery of a drug especially in cancer therapy. The targeting ligand may be a peptide. Examples of targeting peptides are disclosed including cathepsin-D substrate peptides, peptides targeting receptors in the brain and kidney, peptides recognising fibronectin- and vitronectin-binding integrins, peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies, peptides targeting the angiogenic endothelium of solid tumours, tissue specific peptides (e.g. of lung, skin, pancreas, intestine, uterus, adrenal gland and retina), and cationic cancer-targeting peptides. The present sequence is a peptide targeting ligand disclosed in the invent

Qy 1 CVPLTSC 7
Db 1 CLPVASC 7

RESULT 7
 ADC33700 standard; Peptide; 7 AA.
 XX
 ADC33700;
 AC
 XX
 DT 18-DEC-2003 (first entry)
 XX Kidney cell targeted peptide SEQ ID NO:4.
 DE XX chimeric retrovirus envelope protein; ecotropic envelope protein;
 KW cytotoxic; gene therapy; cancer.
 XX
 OS Synthetic.
 XX
 XX WO2003076596-A2.
 PN

Db	1 CLPVASC 7	RESULT 8	ADC33699	ADC33699 standard; peptide; 7 AA.
ID			XX	
AC			AC	ADC33699;
XX			XX	
DT	18-DEC-2003	(first entry)		
DE	Kidney cell targeted peptide SEQ ID NO:3			
XX				
KW	chimeric retrovirus envelope protein; ecotrophic			
KW	cytostatic; gene therapy; cancer.			
XX				
OS	Synthetic.			
XX				
PN	WO2003076596-A2.			
XX				
PD	18-SEP-2003.			
XX				
PP	07-MAR-2003; 2003WO-US007323.			
XX				
PP	08-MAR-2002; 2002US-0362655P.			
XX				

PA (UYMA-) UNIV MASSACHUSETTS.
 XX Green MR, Gollan TJ,
 PI XX WPI; 2003-722332/68.

PT New chimeric retrovirus envelope protein comprising an ectotropic envelope protein and a heterologous short peptide ligand inserted within the ectropic envelope protein useful for treating cancer.

PT Disclosure; SEQ ID NO 3; 42pp; English.

XX The present invention describes a chimeric retrovirus envelope protein comprising an ectropic envelope protein and a heterologous short peptide ligand inserted within the ectropic envelope protein. Also described: (1) a nucleic acid molecule comprising a sequence encoding the recombinant chimeric envelope protein; (2) a vector comprising a nucleic acid sequence encoding the chimeric envelope protein; (3) a recombinant heterologous particle comprising a chimeric envelope protein comprising a heterologous short peptide ligand; (3) altering retroviral tropism; (4) identifying a nucleic acid sequence encoding the chimeric envelope protein that alters viral tropism; (5) delivering a nucleic acid sequence to a cell; and (6) treating cancer. (1) has cytostatic activity and can be used in gene therapy. The chimeric retrovirus envelope protein is useful for treating cancer, which comprises providing a cancer cell, e.g. human cancer cell and infecting the cancer cell with a virus, e.g. retrovirus comprising the chimeric envelope protein comprising a heterologous short peptide ligand and a therapeutically useful gene, e.g. encoding thymidine kinase. The present sequence represents a kidney cell targeted peptide, which is given in the exemplification of the present invention.

Sequence 7 AA;
 SQ 73 .8%; Score 31; DB 7; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPILTSC 7
 Db 1 CLPVASC 7

XX Sequence 6 AA;
 SQ 73 .8%; Score 31; DB 7; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPILT 5
 Db 1 CVPLT 5

RESULT 9
 AAU04531 ABJ00550
 ID AAU04531 standard; peptide; 6 AA.
 AC AAU04531;
 DT 26-SEP-2001 (first entry)
 DE VEGF based monocyclic peptide 9.

XX Human: VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.
 XX Key Disulfide-bond Location/Qualifiers 1..6
 FT /note= "This bond cyclises the peptide"
 XX WO200152875-A1.
 XX 26-JUL-2001.
 XX 18-JAN-2001; 2001WO-US001533.
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX Unidentified.

PA (LUDW-) LUDWIG INST CANCER RES.
 XX Achen MG, Hughes RA, Stacke S, Cendron A;
 PI XX DR WPI; 2001-442248/47.

PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

XX PS Claim 49; Page 32; 102pp; English.

CC The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGF (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-operative restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

XX SQ Sequence 6 AA;

Query Match 69.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPILT 5
 Db 1 CVPLT 5

RESULT 10
 ABJ00550
 ID ABJ00550 standard; peptide; 7 AA.
 AC ABJ00550;
 DT 05-SEP-2002 (first entry)

DE B lymphocyte stimulator protein binding peptide #1.

XX KW B lymphocyte stimulator protein binding protein; BlyS; immune disease; allergy; proliferative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypergammaglobulinaemia; blood clotting; KW ischaemia; graft-versus-host disease; neurodegenerative disease; KW immunosuppressive; nephrotropic; antiarthritic; antiarthritic; KW neuroprotective; cytotropic; immunostimulant; antitumour; anti-HIV; KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic; KW dermatological; antiinflammatory; cardiotonic; ophthalmologic; uropathic; KW antidiabetic; antithyroid; antidepressant; hepatotropic.

DT	02-MAR-2000	(first entry)
KW	rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;	
KW	neurological disease; cyclic.	
Synthetic.		
Homo sapiens.		
Key	Location/Qualifiers	
Disulfide-bond	1..7	
WO957149-A2.		
XX	11-NOV-1999.	
PD	XX	99WO-GA000363.
XX	05-MAY-1999;	99US-00073040.
PR	05-MAY-1998;	98US-00187859.
PR	06-NOV-1998;	98US-00234395.
PR	20-JAN-1999;	99US-00264516.
PR	08-MAR-1999;	99US-00264516.
XX	PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	PA	Blaschuk OW, Gour BJ, Byers S;
XX	PI	WPI: 2000-038791/03.
XX	DR	New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
PS	XX	Claim 48; Page 180; 252pp; English.
CC	XX	The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age -related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AA160592 to AAY64572 represent specifically claimed peptides, and AA164573 to AAY64643 and AA233183 to AAZ33186 represent sequences used in the exemplification of the present invention
CC	XX	Sequence 7 AA;
CC	XX	Sequence 7 AA;
CC	XX	Query Match 59.5%; Score 25; DB 3; Length 7;
CC	XX	Best Local Similarity 57.1%; Pred. No. 1.4e+06;
CC	XX	Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1	CVPLTSC 7
Db	1	CDPKTG 7
SG	Sequence 7 AA;	
Query Match 59.5%; Score 25; DB 3; Length 7;		
Best Local Similarity 57.1%; Pred. No. 1.4e+06;		
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
RESULT 15		
AY62224		
AY62224 standard; peptide; 7 AA.		
XX		
AC		
AAV62224;		
1 CVPLTSC 7		
1 CDPKTG 7		
Query Match 59.5%; Score 25; DB 3; Length 7;		
Best Local Similarity 57.1%; Pred. No. 1.4e+06;		
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
RESULT 16		
AY62224		
AY62224 standard; peptide; 7 AA.		
XX		
AC		
AAV62224;		
1 CVPLTSC 7		
1 CDPKTG 7		
Query Match 59.5%; Score 25; DB 3; Length 7;		
Best Local Similarity 57.1%; Pred. No. 1.4e+06;		
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
RESULT 17		
AY62224		
AY62224 standard; peptide; 7 AA.		
XX		
AC		
AAV62224;		
1 CVPLTSC 7		
1 CDPKTG 7		
Query Match 59.5%; Score 25; DB 3; Length 7;		
Best Local Similarity 57.1%; Pred. No. 1.4e+06;		
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
RESULT 18		
AY62224		
AY62224 standard; peptide; 7 AA.		
XX		
AC		
AAV62224;		
1 CVPLTSC 7		
1 CDPKTG 7		
Query Match 59.5%; Score 25; DB 3; Length 7;		
Best Local Similarity 57.1%; Pred. No. 1.4e+06;		
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		

Sun Sep 5 11:41:01 2004

us-09-761-636a-11.closed.rag

Page 9

Db 1 | | |
 | | |

Search completed: September 5, 2004, 11:17:09
Job time : 64 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:18:40 ; Search time 66 Seconds
(without alignments)

33.416 Million cell updates/sec

Title: US-09-761-636A-11

Perfect score: 42

Sequence: 1 CVPJLSC 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 51522

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 100%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
 1: /cgns_6/ptodata/2/pubpa/us07_PUBCOMB.pep:
 2: /cgns_6/ptodata/2/pubpa/BCT_NEW_PUB.pep:
 3: /cgns_6/ptodata/2/pubpa/us06_NEW_PUB.pep:
 4: /cgns_6/ptodata/2/pubpa/us07_PUBCOMB.pep:
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 13: /cgns_6/ptodata/2/pubpa/us10A_PUBCOMB.pep:
 14: /cgns_6/ptodata/2/pubpa/us10B_PUBCOMB.pep:
 15: /cgns_6/ptodata/2/pubpa/us10C_PUBCOMB.pep:
 16: /cgns_6/ptodata/2/pubpa/us10C_NEW_PUB.pep:
 17: /cgns_6/ptodata/2/pubpa/us60_NEW_PUB.pep:
 18: /cgns_6/ptodata/2/pubpa/us60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	42	100.0	7 9 US-09-761-636A-11	Sequence 11, Appl
2	31	73.8	7 12 US-09-912-609-7	Sequence 7, Appl
3	29	73.8	7 12 US-09-922-227-21	Sequence 21, Appl
4	28	69.0	6 9 US-09-761-636A-12	Sequence 12, Appl
5	28	66.7	7 10 US-09-932-613-8	Sequence 8, Appl
6	28	66.7	7 10 US-09-932-322-8	Sequence 8, Appl
7	26	61.9	7 14 US-10-006-869-1375	Sequence 1375, AP
8	26	61.9	7 15 US-10-006-869-1375	Sequence 1375, AP
9	25	59.5	7 14 US-10-006-869-1799	Sequence 1799, AP
10	25	59.5	7 14 US-10-006-869-3971	Sequence 3971, AP
11	25	59.5	7 14 US-10-006-869-4047	Sequence 4047, AP
12	25	59.5	7 15 US-10-395-032-1799	Sequence 1799, AP
13	25	59.5	7 15 US-10-395-032-33971	Sequence 33971, AP
14	25	59.5	7 15 US-10-395-032-4047	Sequence 4047, AP
15	24	57.1	7 15 US-10-006-869-3574	Sequence 3574, AP
16	24	54.8	7 14 US-10-006-869-1392	Sequence 1392, AP
17	23	54.8	7 14 US-10-006-869-1740	Sequence 1740, AP
18	23	54.8	7 14 US-10-006-869-2155	Sequence 2155, AP
19	23	54.8	7 14 US-10-006-869-2720	Sequence 2720, AP
20	23	54.8	7 14 US-10-006-869-3637	Sequence 3637, AP
21	23	54.8	7 14 US-10-006-869-4041	Sequence 4041, AP
22	23	54.8	7 15 US-10-395-032-1392	Sequence 1392, AP
23	23	54.8	7 15 US-10-395-032-1740	Sequence 1740, AP
24	23	54.8	7 15 US-10-395-032-2155	Sequence 2155, AP
25	23	54.8	7 15 US-10-395-032-7220	Sequence 7220, AP
26	23	54.8	7 15 US-10-395-032-3637	Sequence 3637, AP
27	23	54.8	7 15 US-10-395-032-4041	Sequence 4041, AP
28	23	54.8	7 15 US-10-006-894-35	Sequence 35, APP
29	22	52.4	4 14 US-10-006-869-3621	Sequence 3621, AP
30	22	52.4	7 15 US-09-792-286-221	Sequence 221, APP
31	22	52.4	7 10 US-09-792-286-225	Sequence 225, APP
32	22	52.4	7 14 US-10-006-869-1888	Sequence 1888, APP
33	22	52.4	7 14 US-10-006-869-2750	Sequence 2750, APP
34	22	52.4	7 14 US-10-006-869-3606	Sequence 3606, APP
35	22	52.4	7 14 US-10-006-869-3621	Sequence 3621, APP
36	22	52.4	7 15 US-10-395-032-1888	Sequence 1888, APP
37	22	52.4	7 15 US-10-395-032-2750	Sequence 2750, APP
38	22	52.4	7 15 US-10-395-032-3606	Sequence 3606, APP
39	22	52.4	7 15 US-09-395-032-3621	Sequence 3621, APP
40	21	50.0	6 9 US-09-911-838-1844	Sequence 184, APP
41	21	50.0	6 9 US-09-911-838-186	Sequence 186, APP
42	21	50.0	7 9 US-09-765-006-103	Sequence 103, APP
43	21	50.0	7 9 US-09-911-838-183	Sequence 183, APP
44	21	50.0	7 9 US-09-911-838-185	Sequence 185, APP
45	21	50.0	7 9 US-09-911-838-187	Sequence 187, APP

ALIGNMENTS

RESULT 1
 US-09-761-636A-11 ; Sequence 11, Application US/09761636A
 ; GENERAL INFORMATION:
 ; Patent No. US200200652181
 ; APPLICANT: ACHEN, Marc
 ; STACKER, Steven
 ; HUGHES, Richard
 ; CENDRON, Angela
 ; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
 ; FILE REFERENCE: 1064-48505 Achen et al
 ; CURRENT APPLICATION NUMBER: US 09/761,636A
 ; PRIORITY FILING DATE: 2001-01-18
 ; PRIORITY APPLICATION NUMBER: US 60/176,293
 ; PRIORITY FILING DATE: 2000-05-16
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Version 3.0
 ; SEQ ID NO 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-761-636A-11

Query Match Similarity 100.0%; Score 42; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
 Db 1 CVPLTSC 7

RESULT 2
 US-09-912-609-7 ; Sequence 7, Application US/09912609
 ; Publication No. US20020041898A1

GENERAL INFORMATION:
 APPLICANT: MATSUNAGA, TERRY ONICHI
 APPLICANT: RAMASAMI, VARADARAJAN
 APPLICANT: ROMANSKI, MARK J.
 TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
 FILE REFERENCE: 5030-0001-24
 CURRENT APPLICATION NUMBER: US/09/912,609
 CURRENT FILING DATE: 2001-07-25
 PRIOR APPLICATION NUMBER: 09/703,474
 PRIOR FILING DATE: 2000-10-31
 PRIOR APPLICATION NUMBER: 09/478,124
 PRIOR FILING DATE: 2000-01-05
 NUMBER OF SEQ ID NOS: 131
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 7
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-09-761-636a-7

Query Match 73.8%; Score 31; DB 12; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.2e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
 Db 1 CLPVASC 7

RESULT 3
 US-09-922-227-21
 Sequence 21, Application US/09922227
 Publication No. US20040071689A1
 GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Eiriki
 Pascualini, Renata
 TITLE OF INVENTION: Method of Identifying Molecules That
 Home to a Selected Organ In Vivo
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/922,227
 FILING DATE: 02-Aug-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/526,710
 APPLICATION NUMBER: US 08/195
 APPLICATION NUMBER: US 08/013,273
 FILING DATE: 10-MAR-1997
 APPLICATION NUMBER: US 08/862,855
 FILING DATE: 23-MAY-1997
 APPLICATION NUMBER: US 09/227,906
 FILING DATE: 08-JAN-1999

ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LWJ 4859
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001
 TELEX/FAX: (619) 535-8349
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 21:
 US-09-922-227-21

Query Match 73.8%; Score 31; DB 12; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.2e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
 Db 1 CLPVASC 7

RESULT 4
 US-09-761-636a-12
 Sequence 12, Application US/09761636A
 Patent No. US2004005218A1
 GENERAL INFORMATION:
 APPLICANT: ACHEN, Marc
 APPLICANT: STACKER, Steven
 APPLICANT: HUGHES, Richard
 APPLICANT: CENDRON, Angelia
 TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
 FILE REFERENCE: 1064-4850 Achen et al
 CURRENT APPLICATION NUMBER: US/09/761,636A
 CURRENT FILING DATE: 2001-01-18
 PRIORITY NUMBER: US 60/176,293
 PRIOR FILING DATE: 2000-01-18
 PRIORITY NUMBER: US 60/204,590
 PRIOR FILING DATE: 2000-05-16
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 12
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-761-636a-12

Query Match 69.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVPLT 5
 Db 1 CVPLT 5

RESULT 5
 US-09-932-613-8
 Sequence 8, Application US/09932613
 Publication No. US200309155A1
 GENERAL INFORMATION:
 APPLICANT: Human Genome Sciences, Inc.
 APPLICANT: Beitzer, James P.
 APPLICANT: Potter, M. Daniel
 APPLICANT: Fleming, Tony J.
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
 FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
 CURRENT APPLICATION NUMBER: US/09/932,613
 CURRENT FILING DATE: 2001-08-17
 NUMBER OF SEQ ID NOS: 458
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 8
 LENGTH: 7
 TYPE: PRT

; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
us-10-006-869-1199

Query Match Similarity 59.5%; Score 25; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
Db 1 CDPKTGC 7

RESULT 10
US-10-006-869-3971

; Sequence 3971, Application US/10006869
; Publication No. US20030082166A1

; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS FOR MODULATING NONCLASSICAL

; FILE REFERENCE: 100086_407C9

; CURRENT APPLICATION NUMBER: US/10/395,032

; NUMBER OF SEQ ID NOS: 4052

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 1799

; LENGTH: 7

; TYPE: PRT ; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on

cadherin-12 cell adhesion recognition sequence
US-10-395-032-1799

Query Match Similarity 59.5%; Score 25; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
Db 1 CDPKTGC 7

RESULT 13
US-10-395-032-3971

; Sequence 3971, Application US/10395032
; Publication No. US20030221199A1

; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

; FILE REFERENCE: 100086_407C9

; CURRENT APPLICATION NUMBER: US/10/395,032

; NUMBER OF SEQ ID NOS: 4052

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 3971

; LENGTH: 7

; TYPE: PRT ; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on

cadherin-14 cell adhesion recognition sequence
US-10-395-032-3971

Query Match Similarity 59.5%; Score 25; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
Db 1 CDPKTGC 7

RESULT 14
US-10-395-032-4047

; Sequence 4047, Application US/10006869
; Publication No. US20030082166A1

; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

; FILE REFERENCE: 100086_407C7

; CURRENT APPLICATION NUMBER: US/10/006,869

; NUMBER OF SEQ ID NOS: 4052

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 4047

; LENGTH: 7

; TYPE: PRT ; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on

PB-cadherin cell adhesion recognition sequence
US-10-006-869-4047

Query Match Similarity 59.5%; Score 25; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
Db 1 CDPKTGC 7

Sequence 4047, Application US/10395032
 Publication No. US20030229199A1
 GENERAL INFORMATION:
 APPLICANT: Blaschuk, Orest W.
 APPLICANT: Symonds, James Matthew
 APPLICANT: Gour, Barbara J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL CADHERIN-MEDIATED FUNCTIONS
 FILE REFERENCE: 100086_407C9
 CURRENT APPLICATION NUMBER: US/10/395,032
 CURRENT FILING DATE: 2003-03-21
 NUMBER OF SEQ ID NOS: 4052
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 4047
 LENGTH: 7

TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative cyclic modulating agent based on
 OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
 US-10-395-032-4047

Query Match Similarity 59.5%; Score 25; DB 15; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.2e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CVPLTSC 7
 Db 1 CDPKTG C 7

RESULT 15
 US-10-006-869-3574
 Sequence 3574, Application US/10006869
 Publication No. US20030082166A1
 GENERAL INFORMATION:
 APPLICANT: Blaschuk, Orest W.
 APPLICANT: Symonds, James Matthew
 APPLICANT: Gour, Barbara J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL CADHERIN-MEDIATED FUNCTIONS
 FILE REFERENCE: 100086_407C7
 CURRENT APPLICATION NUMBER: US/10/006,869
 CURRENT FILING DATE: 2001-12-03
 NUMBER OF SEQ ID NOS: 4052
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 3574
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative cyclic modulating agent based on
 OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
 US-10-006-869-3574

Query Match Similarity 57.1%; Score 24; DB 14; Length 7;
 Best Local Similarity 42.9%; Pred. No. 1.2e+06;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CVPLTSC 7
 Db 1 CDPVSGC 7

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OM protein - protein search, using sw model.

Run on: September 5, 2004, 11:16:10 ; Search time 21 Seconds
(without alignments)
17.209 Million cell updates/sec

Title: US-09-761-636A-11

Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs., 51625971 residues

Total number of hits satisfying chosen parameters: 57228

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgns_6/picodata/2/iaa/5b_COMB_pep:*

3: /cgns_6/picodata/2/iaa/6a_COMB_pep:*

4: /cgns_6/picodata/2/iaa/6b_COMB_pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3.1	73.8	7	1 US-09-526-710-21	Sequence 21, App1
2	3.1	73.8	7	3 US-09-862-855-21	Sequence 21, App1
3	3.1	73.8	7	3 US-09-926-985-21	Sequence 21, App1
4	3.1	73.8	7	4 US-09-227-006-21	Sequence 21, App1
5	2.6	61.9	7	4 US-09-187-859-1375	Sequence 1375, App1
6	2.6	61.9	7	4 US-09-839-542B-1375	Sequence 1375, App1
7	2.5	57.5	7	4 US-09-187-859-1799	Sequence 1799, App1
8	2.5	59.5	7	4 US-09-187-859-3971	Sequence 3971, App1
9	2.5	59.5	7	4 US-09-187-859-4047	Sequence 4047, App1
10	2.5	59.5	7	4 US-09-839-542B-1799	Sequence 1799, App1
11	2.5	59.5	7	4 US-09-839-542B-3971	Sequence 3971, App1
12	2.5	59.5	7	4 US-09-839-542B-1047	Sequence 4047, App1
13	2.4	57.1	7	4 US-09-187-859-3574	Sequence 3574, App1
14	2.4	57.1	7	4 US-09-839-542B-2574	Sequence 3574, App1
15	2.3	54.8	6	1 US-07-947-035-13	Sequence 13, App1
16	2.3	54.8	6	1 US-08-321-085A-11	Sequence 11, App1
17	2.3	54.8	7	4 US-09-187-859-1392	Sequence 1392, App1
18	2.3	54.8	7	4 US-09-187-859-1740	Sequence 1740, App1
19	2.3	54.8	7	4 US-09-187-859-2155	Sequence 2155, App1
20	2.3	54.8	7	4 US-09-187-859-2720	Sequence 2720, App1
21	2.3	54.8	7	4 US-09-187-859-3637	Sequence 3637, App1
22	2.3	54.8	7	4 US-09-187-859-4041	Sequence 4041, App1
23	2.3	54.8	7	4 US-09-839-542B-1392	Sequence 1392, App1
24	2.3	54.8	7	4 US-09-839-542B-1740	Sequence 1740, App1
25	2.3	54.8	7	4 US-09-839-542B-2155	Sequence 2155, App1
26	2.3	54.8	7	4 US-09-839-542B-2720	Sequence 2720, App1
27	2.3	54.8	7	4 US-09-839-542B-3637	Sequence 3637, App1

ALIGNMENTS

RESULT 1
US-09-526-710-21
; Sequence 21, Application US/08526710
; Patent No. 5622699
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Method of Identifying Molecules That Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,710
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-526-710-21
Query Match Score 31; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CVPITSC 7
Db 1 CLPVASC 7

RESULT 2
 US-08-862-855-21
 Sequence 21, Application US/08862855
 GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Erkki
 TITLE OF INVENTION: Method of Identifying Molecules That Home to a Selected Organ In Vivo
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 STREET: Campbell & Flores LLP
 ADDRESS: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/226,985
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/526,710
 FILING DATE: 11-SEP-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/813,273
 FILING DATE: 10-MAR-1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/862,855
 FILING DATE: 23-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Kathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LJ 34423
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-226-985-21

Query Match 73.8% Score 31; DB 3; Length 7;
 Best Local Similarity 57.1%; Pred. No. 3e+05; 2; Mismatches 1; Indels 0;
 Gaps 0;

RESULT 4
 US-09-227-906-21
 Sequence 21, Application US/09227906
 GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Erkki
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LJ 26221
 TELEPHONE: (619) 535-9001
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-862-855-21

Query Match 73.8% Score 31; DB 3; Length 7;
 Best Local Similarity 57.1%; Pred. No. 3e+05; 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 3
 US-09-226-985-21
 Sequence 21, Application US/09226985
 GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Erkki
 TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122

COMPUTER READABLE FORM:


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Query Match      59.5%;  Score 25;  DB 4;  Length 7;
Best Local Similarity 57.1%;  Pred. No. 3e+05;  0;  Gaps 0;
Matches 4;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy   1 CVPLTSC 7
Db    1 CDPKTGCG 7

RESULT 9
US-09-187-859-4047
; Sequence 4047, Application US/09187859A
; Patent No. 6359920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086_407D1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 4047
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-187-859-4047

Query Match      59.5%;  Score 25;  DB 4;  Length 7;
Best Local Similarity 57.1%;  Pred. No. 3e+05;  0;  Gaps 0;
Matches 4;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy   1 CVPLTSC 7
Db    1 CDPKTGCG 7

RESULT 10
US-09-839-542B-1799
; Sequence 1799, Application US/09839542B
; Patent No. 6569936
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086_407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1799
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-839-542B-1799

Query Match      59.5%;  Score 25;  DB 4;  Length 7;
Best Local Similarity 57.1%;  Pred. No. 3e+05;  0;  Gaps 0;
Matches 4;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy   1 CVPLTSC 7
Db    1 CDPKTGCG 7

RESULT 11
US-09-839-542B-3971
; Sequence 3971, Application US/09839542B
; Patent No. 6569936
; GENERAL INFORMATION:
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086_407D1
; CURRENT APPLICATION NUMBER: CADHERIN-MEDIATED FUNCTIONS
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3971
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-09-839-542B-3971

Query Match      59.5%;  Score 25;  DB 4;  Length 7;
Best Local Similarity 57.1%;  Pred. No. 3e+05;  0;  Gaps 0;
Matches 4;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy   1 CVPLTSC 7
Db    1 CDPKTGCG 7

RESULT 12
US-09-839-542B-4047
; Sequence 4047, Application US/09839542B
; Patent No. 6569936
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086_407D1
; CURRENT APPLICATION NUMBER: CADHERIN-MEDIATED FUNCTIONS
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 4047
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-839-542B-4047

Query Match      59.5%;  Score 25;  DB 4;  Length 7;
Best Local Similarity 57.1%;  Pred. No. 3e+05;  0;  Gaps 0;
Matches 4;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy   1 CVPLTSC 7
Db    1 CDPKTGCG 7

RESULT 13
US-09-187-859-3574
; Sequence 3574, Application US/09187859A
; Patent No. 6359920
; GENERAL INFORMATION:

```

APPLICANT: Blaschuk, Orest W.
 APPLICANT: Gour, Barbara J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 FILE REFERENCE: 100086-407C1
 CURRENT APPLICATION NUMBER: US/09/187,859A
 CURRENT FILING DATE: 1998-11-06
 NUMBER OF SEQ ID NOS: 4052
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 3574
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative cyclic modulating agent based on
 OTHER INFORMATION: caderin-related neuronal receptor cell adhesion
 US-09-187-859-3574

Query Match Score 24; DB 4; Length 7;
 Best Local Similarity 42.9%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
 Db 1 CDPVSGC 7

RESULT 14
 US-09-839-542B-3574
 / Sequence 3574, Application US/09839542B
 / Patent No. 6569996
 / GENERAL INFORMATION:
 / APPLICANT: Blaschuk, Orest W.
 / APPLICANT: Gour, Barbara J.
 / APPLICANT: Symonds, James Matthew
 / TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 / FILE REFERENCE: 100086-407D1
 / CURRENT FILING DATE: 2001-04-20
 / NUMBER OF SEQ ID NOS: 4052
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 3574
 / LENGTH: 7
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative cyclic modulating agent based on
 OTHER INFORMATION: caderin-related neuronal receptor cell adhesion
 US-09-839-542B-3574

Query Match Score 24; DB 4; Length 7;
 Best Local Similarity 42.9%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
 Db 1 CDPVSGC 7

RESULT 15
 US-09-947-035-13
 / Sequence 13, Application US/07947035
 / Patent No. 5444045
 / GENERAL INFORMATION:
 / APPLICANT: Francis, Geoffrey L.
 / APPLICANT: Walton, Paul E.
 / APPLICANT: Ballard, Francis J.
 / APPLICANT: McMurry, John P.
 / APPLICANT: Phelps, Patricia V.
 / TITLE OF INVENTION: Method of Administering IGF-1, IGF-2,

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C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C;Accession: E60274
 R;Nagai, S.; Wiker, H.G.; Harbore, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991.
 A;Title: Isolation and partial characterization of major protein antigens in the culture
 A;Reference number: A60274; PMID:1698899
 A;Accession: E60274
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <NAG>
 Query Match 36.8%; Score 14; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 PLT 5
 |:
 Db 3 PIT 5
 ||
 2 PL 3

RESULT 4
 F22565
 R-phycoerythrin gamma-A chain - red alga (*Gastroclonium coulteri*) (fragment)
 C;Species: *Gastroclonium coulteri*
 C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
 C;Accession: F22565
 R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
 A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
 A;Reference number: A22565; MUID:85182601; PMID:3886644
 A;Accession: F22565
 A;Molecule type: protein
 A;Residues: 1-5 <RIO>
 Query Match 36.8%; Score 14; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 TC 6
 |||
 Db 2 TC 3
 |||

RESULT 5
 I49421
 Laminin B1 - western wild mouse (fragment)
 C;Species: *Mus spretus* (western wild mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C;Accession: I49421
 R;Ro, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
 A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A;Reference number: 148934; MUID:94319082; PMID:8043949
 A;Accession: I49421
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-6 <RES>
 Query Match 36.8%; Score 14; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 TC 6
 |||
 Db 4 TC 5
 |||

RESULT 6
 A32039
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
 C;Species: *Bos primigenius taurus* (cattle)
 C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000

C;Accession: A32039
 R;Horvath, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989
 A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1
 A;Reference number: A32039; MUID:8912385; PMID:2563371
 A;Accession: A32039
 A;Molecule type: protein
 A;Residues: 1-4 <HOR>
 A;Experimental source: brain
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end
 P;4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.9%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 PL 4
 |||
 Db 2 PL 3

RESULT 7
 I54357
 schwannomin - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C;Accession: I54357
 R;Huynh, D.P.; Nechiporuk, T.; Pulsit, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
 A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are co-expressed
 A;Reference number: 154357; MUID:95072570; PMID:7981675
 A;Accession: I54357
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-4 <RES>
 A;Cross-references: GB:L28838; NID:9454836; PIDN:AAAS57150_1; PID:9601923
 C;Genetics:
 A;Gene: NF2

Query Match 28.9%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 VP 3
 |||
 Db 1 VP 2

RESULT 8
 A60521
 glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (*Liza ramada*) (fragment)
 N;Alternative names: glycogen phosphorylase b
 C;Species: *Liza ramada*
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
 C;Accession: A60521
 R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
 A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
 A;Reference number: A60521; MUID:90227907; PMID:2109669
 A;Accession: A60521
 A;Molecule type: protein
 A;Residues: 1-5 <BON>
 C;Superfamily: glucan phosphorylase
 C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
 C;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim
 Query Match 28.9%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 VP 3
 |||

Db 4 VP 5 Best Local Similarity 50.0%; Pred. No. 2.8e+05; Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
I37263 Y protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C;Accession: I37263
R.Waeber, G.; Habener, J.F.
Endocrinology, 131, 2015, 1992
A;Title: Novel testis germ cell-specific transcript of the CRBB gene contains an alternative
Reference number: I37263; MUID:93010691; PMID:1396344
A;Accession: I37263
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: EMBL:X68994; NID:9396171; PIDN:CAA48780.1; PMID:9579816
C;Generics:
A;Gene: CREB

Query Match Score 11; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 LTC 6
Db 2 LFC 4

RESULT 10
H48394 Glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: H48394
R;Mathew, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.
A;Reference number: A48394; MUID:93250576; PMID:8485470
A;Accession: H48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <RES>
A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBITP:131518)
C;Keywords: Glycoprotein

Query Match Score 11; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 LTC 6
Db 4 LGC 6

RESULT 11
C2255 R-phycocerythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: C2255
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycocerythrin.
A;Reference number: A22555; MUID:85182601; PMID:3886644
A;Accession: C22555
A;Molecule type: protein
A;Residues: 1-6 <KLO>

Query Match Score 10; DB 2; Length 6;
Best Local Similarity 26.3%; Pred. No. 2.8e+05;

RESULT 12
A22565 R-phycocerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycocerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: A22565
A;Molecule type: protein
A;Residues: 1-3 <KLO>

Query Match Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 C 1
Db 1 C 1

RESULT 13
T51049 metallothionein-A - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: T51049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Bur. J. Biochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) metallothionein-A
A;Reference number: I51049; MUID:93324545; PMID:7601121
A;Accession: T51049
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <OQS>
A;Cross-references: EMBL:X80181; NID:g1019799; PID:CAA56466.1; PID:g4379328

Query Match Score 23.7%; Pred. No. 2.8e+05;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 C 1
Db 4 C 4

RESULT 14
S43959 Ig mu chain V region (clone 13) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S43959
R;Wagner, S.D.; Williams, G.T.; Larson, T.; Neuburger, M.S.; Kitamura, D.; Rajewsky, K.;
Nucleic Acids Res. 22, 1389-1393, 1994
A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A;Reference number: S43956; MUID:94248036; PMID:8190629
A;Accession: S43959
A;Molecule type: DNA
A;Residues: 1-4 <WAG>
C;Keywords: immunoglobulin

Query Match Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

	Matches	1;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy		1	C	1						
Db		2	C	2						

RESULT 15

S55238 - pallidipin - assassin bug (fragment)
 C-Species: Triatoma pallidipennis (assassin bug)
 C-IDate: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
 C-Accesion: S55238
 R-Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleuniger, J.; Bloch, J. 307, 465-470, 1995
 A-Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhibitor
 A-Reference number: S55238; MUIID:95251610; PMID:7731884
 A-Accesion: S55238
 A-Molecule type: protein
 A-Residues: 1-4 <HAE>

Query Match Score 9; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

	Matches	1	C	1
Qy		1	C	1
Db		3	C	3

Search completed: September 5, 2004, 11:27:07
 Job time : 21 secs

Result No.	Score	Query	Match	Length	DB ID	Description
1	13	34.2	6	1	E101_LITRU	P82096 litoria rub
2	11	28.9	6	1	VPL9_HSVIK	P23210 herpes simp
3	9	23.7	5	1	E103_LITRU	P19939 litoria rub
4	9	23.7	6	1	CIP2_MYTBD	P13736 mytilus edu
5	9	23.7	6	1	CIP2_MYTBD	P01373 periplaneta americana
6	8	21.1	5	1	PRCT_PERAM	P36414 pseudomonas
7	8	21.1	6	1	TRPL_PEPFU	P01151 suis scrofa
8	7	18.4	3	1	THYL_PIG	P19916 pseudomonas
9	7	18.4	4	1	DCML_PSECH	P36515 saccharomyces cerevisiae
10	7	18.4	4	1	RN01_YEAST	P01858 homo sapien
11	7	18.4	4	1	TUFT_HUMAN	P30425 bothrops innoxius
12	7	18.4	5	1	BIOA_CITFR	P82100 litoria rub
13	7	18.4	5	1	BPP7_BOTIN	P19931 acheta domesticus
14	7	18.4	5	1	E104_LITRU	P42985 leptinotarsa decemlineata
15	7	18.4	5	1	PAP2_PARMA	P14145 sarcophaga
16	7	18.4	6	1	SUGA_ACHDO	P58221 daucus carota
17	7	18.4	6	1	OWM_LBDE	P82072 litoria rub
18	7	18.4	6	1	TWOF_SARBU	P81844 pardachirus paradoxus
19	5	13.2	5	1	PSK_DIAUC	P81321 clostridium perfringens
20	5	13.2	5	1	PE31_LITRU	P81351 clostridium perfringens
21	5	13.2	5	1	RE32_LITRU	P02731 homo sapien
22	5	13.2	6	1	UN06_CLOPA	P42562 hirudo medicinalis
23	4	10.5	4	1	POSI_HUMAN	P58707 anthoplaea anthoplaea
24	4	10.5	4	1	PAR3_HIRME	P81817 carcinus maenas
25	4	10.5	4	1	FLRF_HIRME	P82010 litoria rub
26	4	10.5	4	1	FIRN_ANTEL	P54710 canis familiaris
27	4	10.5	5	1	AL14_CARMA	P80728 zebrasoma mays
28	4	10.5	5	1	RE11_LITRU	P24272 orcytolagus cuniculus
29	4	10.5	5	1	TPIS_CANFA	P24272 vibrio fischeri
30	4	10.5	5	1	UC22_MAIZE	P58706 anthoplaea anthoplaea
31	4	10.5	6	1	ACPH_RABIT	P80728 herpes simplex virus type 1
32	3	7.9	3	1	IUXE_VIBIFI	P80728 papavirus
33	3	7.9	4	1	FYRI_ANTEL	P80728 herpes simplex virus type 1 promoter controlling the

expression of UL38, a true late gene involved in capsid assembly.";
 J. Virol. 65:789-786(1991).

CC -!- COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
 EMBEDDED; BINS DNA.

CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.

CC -----

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CC -----

CC DR ENB1; M57646; ARX45830; 1; -;
 KW Capsid assembly; Coat protein; DNA-binding.
 FT NON_TER 6 AA; 6 MW; 67376451A336F000 CRC64;
 SQ SEQUENCE 6 AA; 703 MW;

Query Match 28.9%; Score 11; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
 Db 5 PL 6

RESULT 3

IDI03_LITRU STANDARD PRT; 5 AA.
 ID BI03_LITRU STANDARD PRT; 5 AA.
 AC P8059;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-OCT-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Electric 3.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Peleodryadinae; Litoria.
 CX NCBI_TaxID=104895;
 RN -----

RP SEQUENCE.

RC TISSUE=Skin secretion;

RA "Peptides from the skin glands of the Australian buzzing tree frog Litoria electrica. Comparison with the skin peptides from Litoria rubella.";
 RT Aust. J. Chem. 52:639-645 (1989).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

KW Amphibian defense peptide; Amidation.

FT MOD_RES 5 AMIDATION;
 SQ SEQUENCE 5 AA; 630 MW; 668761P2C9A00000 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
 Db 4 PM 5

RESULT 4

CIP1_MYTED STANDARD PRT; 6 AA.
 ID CIP1_MYTED STANDARD PRT; 6 AA.
 AC P1373;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)

CC -!- FUNCTION: Inhibitory action on contractions in several molluscan muscles.

CC -!- SIMILARITY: TO MIP II.

CC DR A27696; A27696.
 KW Hormone; Amidation.
 FT MOD_RES 6 AMIDATION;
 SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
 Db 3 PM 4

RESULT 5

CIP2_MYTED STANDARD PRT; 6 AA.
 ID CIP2_MYTED STANDARD PRT; 6 AA.
 AC P13737;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)

CC -!- FUNCTION: Inhibiting peptide II (MIP II).

CC DR B27696; B27696.
 KW Hormone; Amidation.

FT MOD_RES 6 AMIDATION;
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
 Db 3 PM 4

RESULT 6

PRCT_PERAM STANDARD PRT; 5 AA.

ID PRCT_PERAM STANDARD PRT; 5 AA.
 AC P01373;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

CC -!- FUNCTION: Proctolin.

OS Periplaneta americana (American cockroach), and Limulus polyphemus (Atlantic horseshoe crab), and Mytilus edulis (Blue mussel).

OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OX NCBI_TAXID=6978, 6850,
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 MEDLINE=76074708; PubMed=576;
 RX Starratt A.N., Brown B.E.;
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
 in insects.";
 RL Life Sci. 17:1253-1256 (1975).
 RN [2]
 RP BIOLOGICAL SOURCE.
 RC SPECIES=P.americana;
 MEDLINE=90287800; PubMed=2356151;
 RX Groome J.R., Tillinghast B.K., Townley M.A., Vetrov A.,
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
 RA Shabanowitz J.;
 RT "Identification of proctolin in the central nervous system of the
 horseshoe crab, Limulus polyphemus.";
 Peptides 11:205-211(1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=C.maenas;
 MEDLINE=86232789; PubMed=2872661;
 RX Stangler J., Dirksen H., Keller R.;
 RT "Identification and immunocytochemical localization of proctolin in
 pericardial organs of the shore crab, *Carcinus maenas*.";
 RL Peptides 7:67-72(1996).
 -!- FUNCTION: Stimulates cardiac output and hindgut motility,
 CC modulates visceral and skeletal muscle in many arthropods.
 CC -!- TISSUE SPECIFICITY: Found in the lateral white neurons and in
 the crab pericardial organs.
 DR PIR; A01644; HOROHA.
 DR PIR; A60411; A60411.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA: 649 MW: 71B7673B4460000 CRC64;
 Query Match 21.1%; Score 8; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 RN
 RP SEQUENCE.
 ID TRPL_PSEPU STANDARD; PRT;
 AC P36414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE HTH-type transcriptional regulator trpl (trpBA operon transcriptional
 activator) (Fragment).
 GN Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudonadaceae; Pseudomonas.
 OX NCBI_TAXID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PPG1 C1S;

RX MEDLINE=89335826; PubMed=2503057;
 RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of *Pseudomonas*
 putida";
 RL Biochimie 71:521-531(1999).
 -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
 CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
 CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
 CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 -!- SIMILARITY: Contains 1 HTH LYR-type DNA-binding domain.
 CC
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 CC
 DR EMBL; X13299; CAA3160_1;
 DR InterPro; IPR00847; HTH_DysR.
 DR PROSITE; PS50931; HTH_LYSN; PARTIAL.
 RC KW TRYPTOPHAN biosynthesis; Transcription regulation; Activator;
 RA KW DNA-binding.
 FT NON-TER 6 6
 SQ SEQUENCE 6 AA: 683 MW: 77672AA1EDD6F000 CRC64;
 Query Match 21.1%; Score 8; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 RN
 RESULT 8
 THYL_PIG
 ID THYL_PIG
 AC P01151;
 STANDARD; PRT;
 AC P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Thyrocalcitonin (Thyrotropin releasing hormone) (TRH) (Protirelin).
 OS Sus scrofa (Pig),
 OS Ovis aries (Sheep),
 OS Bombina orientalis (Oriental fire-bellied toad), and
 OS *Notophthalmus viridescens* (Eastern newt) (*Triturus viridescens*)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cerartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9023, 9940, 8346, 8316;
 RN [1]
 RP SEQUENCE.
 SPECIES=Fig; TISSUE=Hypothalamus;
 RX MEDLINE=70136150; PubMed=4984938;
 RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
 RT "Structure of porcine thyrotropin releasing hormone.";
 RL Biochemistry 9:1103-1106(1970).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=Fig;
 RX MEDLINE=10039904; PubMed=4982117;
 RA Boier J., Fuzmann F., Folkers K., Bowers C.Y., Schally A.V.;
 RT "The identity of chemical and hormonal properties of the thyrotropin
 releasing hormone and pyroglutamyl-nistidyl-proline amide.";
 RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Hypothalamus;
 RA Desiderio D.M. Jr., Burgs R., Dunn T.F., Vale W., Guillemin R.,
 RA Ward D.N.;
 RT "The elucidation of the primary structure of the hypothalamic thyroid
 stimulating hormone releasing factor of ovine origin by means of mass

RT spectrometry.";
 Org. Mass Spectrom. 5:221-228(1971).
 RN [4].

RP SYNTHESIS.
 RC SPECIES="Sheep"; PubMed=4985794;
 RX MEDLINE=70163386; PubMed=4985794;
 RA Burgs R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
 RA Guillemin R.;
 RT "Characterization of ovine hypothalamic hypophysiotropic
 TSH-releasing factor.";
 RT Nature 226:321-325(1970);
 RL [5].

RN SEQUENCE.
 SPECIES=B.Orientalis; TISSUE=Skin;
 RX MEDLINE=76138399; PubMed=915011;
 RA Yasuhara T., Nakajima T.;
 RT Letter: Occurrence of Pyr-His-Pro-NH₂ in the frog skin.";
 RL Chem. Pharm. Bull. 23:3301-3303(1975).
 RN [6].

RN SEQUENCE.
 SPECIES=N.Viridecescens; PubMed=4214528;
 RX MEDLINE=75035605; PubMed=4214528;
 RA Grimm-Jorgensen Y., McKelvy J.F.;
 RT "Biogenesis of thyrotropin releasing factor by new (Triturus
 viridecescens) brain in vitro. Isolation and characterization of
 thyrotropin releasing factor.";
 RT J. Neurochem. 23:471-478(1974).
 CC FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 in the anterior pituitary gland and as a neurotransmitter/
 neuromodulator in the central and peripheral nervous systems.
 DR PIR: A90919; RHTDPO.
 DR PIR: A92971; A92971.
 KW Amidation; Pyrrolidine carboxylic acid.
 FT PYRROLIDONE CARBOXYLIC ACID.
 MOD_RES 1 1
 MOD_RES 3 3
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 18.4%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 P 3
 DB 3 P 3

RESULT 9
 DCML_PSECH
 ID DCML_PSECH
 STANDARD; PRT; 4 AA.

AC P19376;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN CDTL.
 OS Pseudomonas carboxydehydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN [1].

RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 carboxydrophic bacteria";
 RT Arch. Microbiol. 152:335-341 (1989).
 RL -I- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 dioxide.
 CC -I- CATALYTIC ACTIVITY: CO + H₂O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -I- COFACTOR: Molybdenum (molybdopterin).

CC -I- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 SMALL.
 DR PIR: PI0140; PI0140.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 18.4%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 P 3
 DB 4 P 4

RESULT 10
 RM01_YEAST
 ID RM01_YEAST
 STANDARD; PRT; 4 AA.

AC P36515;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Mitochondrial 60S ribosomal protein L1 (yml1) (Fragment).
 GN MRPL1.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetidae; Saccharomyces.
 OC Saccharomyctales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1].

RP SPECQUENCE.
 RX MEDLINE=91285106; PubMed=2060626;
 RA Grichmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal
 subunit from yeast mitochondria.";
 RT FEBS Lett. 284:51-56 (1991).
 RL PIR: S17255; S17255.
 DR SGD; L0002681; MRPL1.
 DR NCBI_TaxID=9606;

Query Match 18.4%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 P 3
 DB 4 P 4

RESULT 11
 TUFT_HUMAN
 ID TUFT_HUMAN
 STANDARD; PRT; 4 AA.

AC P01658;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Phagocytosis-stimulating peptide (Tuftsin).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1].

RP SEQUENCE.
 RX MEDLINE=72187087; PubMed=4112769;
 RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
 RT "The characteristics, isolation and synthesis of the phagocytosis
 stimulating peptide tuftsin.";
 RT Biochem. Biophys. Res. Commun. 47:172-179 (1972).
 RL [2].

RP IMMUNOGLOBULIN CLASS.

RX MEDLINE=68091045; PubMed=4169272;

RA Fidalgo B.V.; Najjar V.A.;

RT "the physiological role of the lymphoid system. VI. The stimulatory effect of leucophilic gamma globulin (leucokinin) on the phagocytic activity of human polymorphonuclear leucocyte.";

RL Biochemistry 6:3386-3392 (1987).

-!- CC MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the cell membrane of neutrophils in the blood. Leukokinase on the membrane releases the active peptide tuftsin from the gamma chain.

CC Tuftsin is essential for maximum stimulation of the phagocytic activity of neutrophils.

DR PIR; A0147; A02147.

DR MIM; 191150; -.

DR GO; GO:003023; P: antigen binding; NAS.

DR GO; GO:0065909; P: phagocytosis; NAS.

SEQUENCE 4 AA; 501 MW; 74176321C000000 CRC64;

Query Match Score 7; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3

Db 3 P 3

RESULT 12

BIOA_CITER_ID BIOA_CITER STANDARD; PRT; 5 AA.

AC P13071; P13071; Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-JAN-1990 (Rel. 13, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Adenomethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62) ('7,8-diamino-pelargonic acid aminotransferase) (DAPA aminotransferase) (Fragment).

DE PIR; G37196; G37196.

GN Citrobacter freundii

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Citrobacter.

OX NCBI_TaxID=546; [1] _TAXID=546;

RN PIR_N.A.; SEQUENCE FROM N.A.

RX MEDLINE=B9006280; PubMed=2971595;

RA Shiuhan D.; Campbell A.;

RT "Transcriptional regulation and gene arrangement of Escherichia coli Citrobacter freundii and Salmonella typhimurium biotin operons.";

RL Gene 67:203-211(1988).

-!- CC CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanate + 7,8-diaminononanoate.

CC -!- COFACTOR: Pyridoxal phosphate.

CC -!- PATHWAY: Biotin biosynthesis.

CC -!- SUBUNIT: Homodimer.

CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent aminotransferases.

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CC

DR EMBL; M21922; -; NOT_ANNOTATED_CDS.

DR PIR; I40697; I40697.

DR InterPro; IPR005814; Aminotrans_3.

DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.

KW Biotin biosynthesis; Transferase; Aminotransferase;

KW Pyridoxal phosphate.

FT NON_TER 5 AA; 582 MW; 6AAABIB1A6P00000 CRC64;

SQ SEQUENCE 5 AA; 582 MW; 6AAABIB1A6P00000 CRC64;

Query Match Score 7; DB 1; Length 5;

Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LT 5

Db 1 MT 2

RESULT 13

BPP7_BOTTIN STANDARD; PRT; 5 AA.

ID BPP7_BOTTIN

AC P30425;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide S5_{1,2} (5A) (Angiotensin-converting enzyme inhibitor).

OS Bothrops insularis (Island jararaca) (Quemada jararaca).

OC Lekaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Oviparidae; Crotalinae; Bothrops.

OC Squamata; Scleroglossa; Serpentes; Colubroidea;

OC VIPERIDAE; Crotalinae; Bothrops.

NCBI_TaxID=8723; [1]

RN RP SEQUENCE.

RC TISSUE_VENOM;

RX MEDLINE=90351557; PubMed=2386615;

RA Cintra A.C.O Vieira C.A.; Giglio J.R.;

RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";

J. Protein Chem. 9:221-227(1990)

-!- CC FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.

CC It acts as an indirect hypotensive agent.

DR PIR; G37196; G37196.

KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD_PBS 1 PIRYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match Score 7; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3

Db 5 P 5

RESULT 14

EI04_LITRU STANDARD; PRT; 5 AA.

ID EI04_LITRU

AC P82170;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB Electrin 4.

OS Litoria rubella (Desert tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; Pelodryadinae; Litoria.

NCBI_TaxID=104995; [1]

RN RP SEQUENCE.

RC TISSUE=Skin secretion;

RA Wabnitz P.A.; Bowie J.H.; Tyler M.J.; Wallace J.C.;

RT "Peptides from the skin glands of the Australian buzzing tree frog Litoria electrica. Comparison with the skin peptides from Litoria rubella.";

RT Aust. J. Chem. 52:639-645 (1999).

RL CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

KW Amphibian defense peptide; Amidation.
 FT MOD_RES 5 5 MW; 616 MW; 61FDIAU59A00000 CRC64;
 SQ SEQUENCE 5 AA; :|:
 Query Match 18.4%; Score 7; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 LT 5
 Db 2 IT 3

RESULT 15

PPAP2_PARMA	PAP2_PARMA	STANDARD;	PRT;	5 AA.
ID P81874;				
AC P81874;				
DT 30-MAY-2000 (Rel. 39, Created)				
DT 30-MAY-2000 (Rel. 39, Last sequence update)				
DT 28-FEB-2003 (Rel. 41, Last annotation update)				
DE Pardaxin II (PXII) (Fragment).				
OS Pardachirus marmoratus (Red sea moses sole).				
BUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Neoteleosteii;				
OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;				
OC Soleiidae; Soleidae; Pardachirius.				
NCBI_TAXID=31087;				
RN [1]				
RP SEQUENCE.				
RC TISSUE=Skin secretion;				
RE MEDLINE=7057369; PubMed=3782138;				
RA Lazarovici P., Primor N., Loew L.M.;				
RT "Purification and pore-forming activity of two hydrophobic polypeptides from the secretion of the Red sea moses sole (Pardachirus marmoratus)"				
RT J. Biol. Chem., 261:16704-16713 (1986)				
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant properties. Forms voltage-dependent, ion-permeable channels in membranes. At high concentration causes cell membrane lysis.				
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.				
CC -!- SUBCELLULAR LOCATION: Secreted.				
CC -!- SIMILARITY: Belongs to the pardaxin family.				
KW				
FT NON_TER 5 5 MW; 614 MW; 7769C9C9C8100000 CRC64;				
SQ SEQUENCE 5 AA; : : Query Match 18.4%; Score 7; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 3 P 3 Db 5 P 5				

Search completed: September 5, 2004, 11:25:35
 Job time : 16 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:22:21 ; Search time 58 Seconds

(without alignments) 32.640 Million cell updates/sec

Title: US-09-761-636A-12
Perfect score: 38
Sequence: [1] CVPLTC 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5
Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 11

Minimum DB seq length: 0

Maximum DB seq length: 6
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_rbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodont:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	12	31.6	5	13	P83308	P83308 gallus gallus	
2	9	23.7	6	5	P83569	P83569 sepiia officinalis	
3	5	13.2	5	2	P83073	P83073 bacillus cereus	
4	5	13.2	6	2	P83533	P83533 lactobacillus	
5	5	13.2	6	10	P82181	P82181 spinacia oliveriana	
6	6	13.2	6	10	P82541	P82541 spinacia oliveriana	
7	5	13.2	6	10	P82182	P82182 spinacia oliveriana	
8	4	10.5	4	5	P83568	P83568 sepiia officinalis	
9	4	10.5	4	11	Q80433	Q80433 rattus species	
10	2	5.3	5	10	Q99007	Q99007 hordeum vulgare	
11	0	0.0	2	5	P83570	P83570 sepiia officinalis	

RESULT 1	P83308	PRELIMINARY;	PRT;	5 AA.
ID	P83308;			
AC	P83308;			
DT	01-JUN-2002 (TREMBLref).	21; Created		
DT	01-JUN-2002 (TREMBLref).	21; Last sequence update		
DT	01-JUN-2003 (TREMBLref).	24; Last annotation update		
DE	FMRamide-like neuropeptide (LPFLRF-amide).			
OS	Gallus gallus (chicken)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianae; Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE, AND SYNTHESIS.			
RC	TISSUE;Brain;			
RX	PubMed:6137771;			
RA	Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.; "A novel active pentapeptide from chicken brain identified by antibodies to FMRFamide"; Nature 205:328-330 (1993).			
RT	-!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.			
CC	-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.			
DR	GO:0007218; P:neuropeptide signaling pathway; TAS.			
KW	Neuropeptide; Amidation.			
FT	MOD_RES	5	AMIDATION.	
SQ	SEQUENCE	5 AA;	645 MW;	69D4073767400000 CRC64;
Query Match	31.6%	Score 12;	DB 13;	Length 5;
Best Local Similarity	66.7%	Pred. No. 1e+00;		
Matches	2;	Conservative 1;	Mismatches 0;	Gaps 0;
Qy	2 VPL 4			
Db	:	1 LPL 3		
RESULT 2	P83569	PRELIMINARY;	PRT;	6 AA.
ID	P83569;			
AC	P83569;			
DT	01-JUN-2003 (TREMBLref).	24; Created		
DT	01-JUN-2003 (TREMBLref).	24; Last sequence update		
DB	sperm attracting peptide SepAP.			
OS	Eukaryota; Metazoa; Molluscs; Cephalopoda; Coleoidea; Neocoelioidea; Decapodiformes; Sepioidae; Sepiidae; Sepia.			
NCBI_TaxID=6610;				
RN	[1]			
RP	SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND AMIDATION.			
RC	AMIDATION.			
TISSUE=Egg;				
RX	PubMed:1207899;			
RA	Zatyni C., Marvin L., Gagnon J., Henry J.; "Fertilization in Sepia officinalis: the first mollusk sperm-attracting peptide."; Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).			
RT	-!- FUNCTION: ATTRACTS SPERM INCREASING THE CHANCES OF GAMETE COLLISION.			
CC	-!- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE OVARIAN FOLLICLES DURING FERTILIZATION. EXPRESSION CONTINUES IN THE SECRETED EGGS CAPSULE AFTER FERTILIZATION.			
CC	ACCUMULATES IN THE EGG CAPSULE AFTER FERTILIZATION.			
CC	-!- MASS SPECTROMETRY: MW=59.6 ; METHOD=MALDI.			
FT	MOD_RES	6	AMIDATION.	
SQ	SEQUENCE	6 AA;	597 MW;	72C8676A0470000 CRC64;
Query Match	23.7%	Score 9;	DB 5;	Length 6;
Best Local Similarity	50.0%	Pred. No. 1e+00;		
Matches	1;	Conservative 1;	Mismatches 0;	Gaps 0;

ALIGNMENTS

QY	3 PL 4 1 PI 2	P83073	PRELIMINARY;	PRT;	5 AA.	
DB		ID P83073; AC P83073; DT 01-OCT-2001 [TREMBLrel. 18, Created] DT 01-JUN-2003 [TREMBLrel. 18, Last sequence update] DT 01-OCT-2003 [TREMBLrel. 25, Last annotation update] DB 88 kDa protein (Fragment). OS <i>Bacillus cereus</i> . OC Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> . NCBI_TaxID=1396; RN [1] RP SEQUENCE. RC STRAIN=NCFB 11796; RA Brown N.; Dowds B.C.A.; RL Submitted (JUL-2001) to Swiss-Prot. FT NON_TER: 5 MW: 5 SEQUENCE 5 AA; 623 MW; SQ 6B01AAA336F00000 CRC64;				
Qy	5 T 5 4 T 4	Query Match Best Local Similarity 100.0%; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Score 5; DB 2; Length 5; Pred. No. 1e+06;			
Db						
RESULT 3	P83073	PRELIMINARY;	PRT;	5 AA.		
DT 01-JUN-2000 [TREMBLrel. 14, Created] DT 01-JUN-2000 [TREMBLrel. 14, Last sequence update] DT 01-OCT-2003 [TREMBLrel. 25, Last annotation update] DB Chloroplast 50S ribosomal protein L10 beta (Fragment). OS <i>Spinacia olaracea</i> (Spinach). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Spinacia. NCBI_TaxID=3562;	OX NCBI_TaxID=3562; RN [1] RP SEQUENCE. RC STRAIN=CV; ALWARO; TISSUE=Leaf; AC P83073; DT 01-OCT-2001 [TREMBLrel. 18, Last sequence update] DT 01-JUN-2003 [TREMBLrel. 25, Last annotation update] DB 88 kDa protein (Fragment). OS <i>Bacillus cereus</i> . OC Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> . NCBI_TaxID=1396; RN [1] RP SEQUENCE. RC STRAIN=NCFB 11796; RA Brown N.; Dowds B.C.A.; RL Submitted (JUL-2001) to Swiss-Prot. FT NON_TER: 5 MW: 5 SEQUENCE 5 AA; 623 MW; SQ 6B01AAA336F00000 CRC64;					
Qy	5 T 5 4 T 4	Query Match Best Local Similarity 100.0%; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Score 5; DB 10; Length 6; Pred. No. 1e+06;			
Db						
RESULT 4	P83533	PRELIMINARY;	PRT;	6 AA.		
DT 01-JUN-2003 [TREMBLrel. 24, Created] DT 01-JUN-2003 [TREMBLrel. 24, Last sequence update] DT 01-JUN-2003 [TREMBLrel. 24, Last annotation update] DB Unknown Protein From 2D-page (Fragment). OS Lactobacillus <i>santafrciscensis</i> (Lactobacillus <i>santfrancisco</i>). OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; NCBI_TaxID=1625; RN [1] RP SEQUENCE. RC STRAIN=DSM 20451; RX PubMed=12112660; RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.; RT "High pressure effects step wise altered protein expression in Lactobacillus <i>santfranciscensis</i> ." RT Proteomics 2:765-774 (2002). CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 15 kDa. NON_TER 1 FT 1 MW: 15 kDa; SEQUENCE 6 AA; 590 MW; SQ 6DDDD452D1AAC000 CRC64;						
Qy	5 T 5 2 T 2	Query Match Best Local Similarity 100.0%; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Score 5; DB 2; Length 6; Pred. No. 1e+06;			
Db						
RESULT 5	P82181	PRELIMINARY;	PRT;	6 AA.		
DT P82181 AC						

DR	GO;GO-0003735; F:structural constituent of ribosome; IEA.	RP	SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
DR	InterPro; IPR002222; Ribosomal S19.	RP	"Fertilization in Sepia officinalis: the first mollusk sperm-attracting peptide."
KW	Ribosomal protein; Chloroplast; rRNA-binding.	RC	Zatyni C., Gagnon J., Boucaud-Camou E., Henry J.; Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).
FT	NON-TER 6 AA;	RA	-!- FUNCTION: HAS MYOTROPIC ACTIVITY TARGETING THE GENITAL TRACT.
SQ	SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;	RT	-!- TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OCOCYTE AND EGG (EC2).
	Query Match Best Local Similarity 13.2%; Score 5; DB 10; Length 6; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RL	-!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI.
Qy	5 T 5	RR	Pheromone. DR GO; GO:0005186; F:pheromone activity; IEA.
Db	1 T 1	RN	SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;
	PRELIMINARY; PRT; 6 AA.	RP	SEQUENCE=Bg; TISSUE=Bg; Published=12207899;
ID	P82182	RA	Zatyni C., Marvin L., Gagnon J., Henry J.; Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).
AC	P82182;	RT	-!- FUNCTION: HAS MYOTROPIC ACTIVITY TARGETING THE GENITAL TRACT.
DT	01-JUN-2000 (TREMBLrel. 14; Last sequence update)	CC	-!- SUBCELLULAR LOCATION: SECRETED.
DT	01-JUN-2000 (TREMBLrel. 14; Last annotation update)	CC	-!- TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OCOCYTE AND EGG (EC2).
DT	01-OCT-2003 (TREMBLrel. 25; Last annotation update)	CC	-!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI.
DB	Chloroplast 50S ribosomal protein L10 gamma (Fragment).	DR	GO; GO:0005186; F:pheromone activity; IEA.
OS	Spinacia oleracea (Spinach).	DR	Pheromone. KW
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicots; core eudicots; Caryophyllales; Amaranthaceae; Spinacia.	DR	SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;
OC	NCBI_TaxID=3562;	Qy	Query Match Best Local Similarity 10.5%; Score 4; DB 5; Length 4; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RN	[1]	Db	4 I 4
RP	SEQUENCE.	DB	2 L 2
RC	STRAIN_CV: ALWARO; TISSUE=Leaf;		
RC	MEDLINE=20435798; PubMed=10874046;		
RX	Yamaguchi K., Subramanian A.R.; RT "The Plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast)", J. Biol. Chem. 275:28466-28482(2000).	RESULT 9	PRELIMINARY; PRT; 4 AA.
RA	RT "The Plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast)", J. Biol. Chem. 275:28466-28482(2000).	Q08433	PRELIMINARY; PRT; 4 AA.
CC	-!- FUNCTION: THIS PROTEIN BELONGS DIRECTLY TO 23S RIBOSOMAL RNA.	AC	Q08433; PRELIMINARY; PRT; 4 AA.
CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST.	DT	01-NOV-1996 (TREMBLrel. 01; Created)
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.	DT	01-NOV-1996 (TREMBLrel. 01; Last sequence update)
CC	-!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.	DT	01-JUN-2003 (TREMBLrel. 24; Last annotation update)
CC	-!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.	DE	Billirubin UDP-glucuronosyltransferase (Fragment).
GO	GO:0005507; C:chloroplast; IEA.	OS	Rattus sp.; Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathini; Muridae; Murinae; Rattus.
GO	GO: GO:0019843; P:rRNA binding; IEA.	OC	NCBI_TaxID=10118;
GO	GO: GO:0003735; F:structural constituent of ribosome; IEA.	OX	RN [1] SEQUENCE FROM N.A.
DR	InterPro; IPR002363; Ribosomal L10a.	RP	SEQUENCE FROM N.A.
DR	PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.	RC	STRAIN=Gunn;
KW	Ribosomal Protein; Chloroplast; rRNA-binding.	RX	MEDLINE=912822758; PubMed=1840486;
FT	NON-TER 6 AA;	RA	Sato H., Aono S., Kashiwamoto S., Koiwai O.; "Genetic defect of billirubin UGP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat." Biochem. Biophys. Res. Commun. 177:1161-1164 (1991).
SQ	SEQUENCE 6 AA; 675 MW; 6321B415B05D800 CRC64;	DT	DR EMBL; S38636; AB19239.1; "
	13.2%; Score 5; DB 10; Length 6; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	F:transferase activity; IEA.
Qy	5 T 5	FW	Transferase.
Db	5 T 5	FT	NON-TRR 1 1
	PRELIMINARY; PRT; 4 AA.	SQ	SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;
	13.2%; Score 5; DB 10; Length 6; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	Query Match Best Local Similarity 10.5%; Score 4; DB 11; Length 4; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
P83568	PRELIMINARY; PRT; 4 AA.	Db	2 V 2
ID	P83568;		2 V 2
AC	P83568;		
DT	01-JUN-2003 (TREMBLrel. 24; Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24; Last annotation update)		
DE	Pheromone peptide IIME.		
OS	Sepia officinalis (Common cuttlefish).		
OC	Bukaryota; Metazoa; Mollusca; Coleoidea; Neocoelioidea; Decapodiformes; Sepioidae; Sepiidae.		
OC	Decapodiformes; Sepioidae; Sepiidae.		
OX	NCBI_TaxID=6610;		
	RESULTS 8		
P83568	PRELIMINARY; PRT; 4 AA.		
ID	P83568;		
AC	P83568;		
DT	01-JUN-2003 (TREMBLrel. 24; Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24; Last annotation update)		
DE	Pheromone peptide IIME.		
OS	Sepia officinalis (Common cuttlefish).		
OC	Bukaryota; Metazoa; Mollusca; Coleoidea; Neocoelioidea; Decapodiformes; Sepioidae; Sepiidae.		
OC	Decapodiformes; Sepioidae; Sepiidae.		
OX	NCBI_TaxID=6610;		
	RESULTS 10		
Q99007	PRELIMINARY; PRT; 5 AA.		
TD	Q99007;		
AC	Q99007;		
DT	01-NOV-1996 (TREMBLrel. 01; Created)		

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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:19:05 ; Search time 62 Seconds
(without alignments)

Title: US-09-761-636A-12

Perfect score: 38 CVPLTC 6

Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 28547505 residues

Total number of hits satisfying chosen parameters: 59163

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: GeneseqP1980s:*
- 2: GeneseqP1990s:*
- 3: GeneseqP2000s:*
- 4: GeneseqP2001s:*
- 5: GeneseqP2002s:*
- 6: GeneseqP2003as:*
- 7: GeneseqP2003bs:*
- 8: GeneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	38	100.0	6	4 AAU04531	Aau0531 VEGF base
2	26	68.4	6	3 AY61488	Aay61488 Cadherin-
3	25	67.8	6	3 AY62223	Aay62223 Cadherin-
4	25	65.8	6	3 AY62163	Aay62163 PB-cadherin
5	25	65.8	6	3 AY62006	Aay62006 Cadherin-
6	24	63.2	6	3 AY64259	Aay64259 Cadherin-
7	23	60.5	6	3 AY85373	Aay85373 IL-2 deri
8	23	60.5	6	3 AY62577	Aay62577 PB-cadherin
9	23	60.5	6	3 AY62488	Aay62488 Cadherin-
10	23	60.5	6	3 AY4431	Aay4431 Peptide 1
11	22	57.9	4	2 AAR15772	Aar15772 Farnesy1
12	22	57.9	4	2 AAR49769	Aar49769 Farnesy1
13	22	57.9	4	2 AAR77833	Aar77833 Farnesy1
14	22	57.9	4	2 AAW04459	Aaw04459 Farnesy1
15	22	57.9	5	2 AAW67428	Aaw67428 HCV Pepti
16	22	57.9	6	2 AAW31456	Aaw31456 Transcript
17	22	57.9	6	3 AY61235	Aay61235 Protocad
18	21	57.9	6	3 AY61927	Aay61927 Cadherin-
19	21	55.3	6	3 AY62132	Aay62132 Cadherin-
20	21	55.3	6	3 AY63263	Aay63263 Protocad
21	20	52.6	4	2 AAR51652	Aar51652 Osteogenin
22	20	52.6	5	2 AAR08270	Aar08270 Peptide 1
23	20	52.6	5	2 AAR18749	Aar18749 Glycosyla
24	20	52.6	5	3 AY69213	Aay69213 Peptide f
25	20	52.6	5	3 AY56095	Aay56095 Glycohaem

ALIGNMENTS

RESULT 1
ID AAU04531 standard; peptide; 6 AA.
XX AC AAU04531;
XX DT 26-SEP-2001 (first entry)
XX DE VEGF based monocyclic peptide 9.
XX Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
XX KW Synthetic.
FH Key Location/Qualifiers
FT Disulfide-bond 1..6
ET /note= "This bond cyclises the peptide"
XX XX

WO200152875-A1
XX PD 26-JUL-2001.
XX PF 18-JAN-2001; 2001WO-US001533.
XX PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-024590P.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Achen MG, Hughes RA, Stackler S, Cendron A;
XX DR 2001-442248/47.
XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
XX PT The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human, VBGF (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a

peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vessels. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

Sequence 6 AA:

Query Match	100.0%	Score 38;	DB 4;	Length 6;
Best Local Similarity	100.0%	Prod. No. 1.4e+06;	Indels 0;	Gaps 0;
Matches	6;	Conservative 0;	Mismatches 0;	
QY	1 CVPKTC 6			
DB	1 CVPKTC 6			

RESULT 2
AYA1488 standard; peptide; 6 AA.

XN AAY1488;

AC

XX

DT 02-MAR-2000 (first entry)

DE Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1374.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR; KW inhibition; cadherin extracellular domain; cell adhesion recognition; KW OB-cadherin; cadherin-5; cadherin-7; cadherin-8; cadherin-12; KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin; KW cadherin related neuronal receptor; Li-cadherin; protocadherin; KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity; KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; KW neurological disease; cyclic.

XX OS Homo sapiens.

OS Synthetic.

XX PF 05-MAY-1999; 98WO-A000063.

XX PR 05-MAY-1998; 98US-00073040.

PR 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.

PR 08-MAR-1999; 99US-00264516.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

PI

XX WPI; 2000-038791/03.

DR New cadherin modulating agents, used for modulating nonclassical cadherin PT-mediated functions for treating e.g. cancers, obesity, rheumatoid PT arthritis, multiple sclerosis, diabetes or a neurological disease.

XX Claim 36; Page 172; 252pp; English.

XX The present invention describes Cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vaso permeability in a mammal, enhancing synaptic stability in nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating adhesion of foreign tissue in a scar tissue, or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AA160592 to AAY64572 represent specifically claimed peptides, and AA164573 to AAY64643 and AA233183 to AA233186 represent sequences used in the exemplification of the present invention.

SQ Sequence 6 AA;

Query	Match	68.4%; Score 26;	DB 3;	Length 6;
ID	AYA1488	Best Local Similarity 66.7%;	Prod. No. 1.4e+06;	
Match	4;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 CVPKTC 6			
Db	1 CVPKTC 6			

XX Sequence 6 AA;

Query	Match	68.4%; Score 26;	DB 3;	Length 6;
ID	AYA1488	Best Local Similarity 66.7%;	Prod. No. 1.4e+06;	
Match	4;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 CVPKTC 6			
Db	1 CVPKTC 6			

XX Sequence 6 AA;

Query	Match	68.4%; Score 26;	DB 3;	Length 6;
ID	AYA1488	Best Local Similarity 66.7%;	Prod. No. 1.4e+06;	
Match	4;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 CVPKTC 6			
Db	1 CVPKTC 6			

XX Sequence 6 AA;

RESULT 3
AYA1488 standard; peptide; 6 AA.

XX ID AAY62223

XX ID AAY62223 standard; peptide; 6 AA.

XX AC AAY62223;

XX AC AAY62223;

XX DT 02-MAR-2000 (first entry)

DE Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3970.

XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;

KW inhibition; cadherin extracellular domain; cell adhesion recognition;

KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;

KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;

KW cadherin related neuronal receptor; Li-cadherin; protocadherin;

KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;

KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;

KW neurological disease; cyclic.

XX OS Synthetic.

XX OS Homo sapiens.

XX PR 05-MAY-1999; 98US-A000063.

XX PR 05-MAY-1998; 98US-00073040.

PR 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.

PR 08-MAR-1999; 99US-00264516.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuk OW, Gour BJ, Byers S;

PI

XX Key Disulfide-bond 1..6

XX FT Disulfide-bond 1..6

XX PN WO9957149-A2.

XX PD 11-NOV-1999.

XX XX

XX OS Synthetic.

XX OS Homo sapiens.

XX PR

XX PH

XX FT

XX PN

XX DE

XX XX

XX XX

XX PR

XX PH

XX FT

XX PN

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PF 05-MAY-1999; 99WO-CA000363.
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX PI Biaschuk OW, Gour BJ, Byers S;
 XX DR WPI; 2000-038791/03.
 XX PT New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX PS Claim 54: Page 184: 252pp; English.
 XX CC The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumor in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vaso permeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age -related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAY64572 represent specifically claimed peptides, and AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in the exemplification of the present invention
 XX SQ Sequence 6 AA;
 Query Match 65.8%; Score 25; DB 3; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CVPLTC 6
 Db 1 CDPKTC 6

RESULT 4
 AAY62763 standard; peptide; 6 AA.
 ID AAY62763
 XX AC AAY62763;
 DT 02-MAR-2000 (first entry)
 DE PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4046.
 XX KW Modulation; nonclassical-cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; P-cadherin;
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 XX DE Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:1798.

OS Synthetic.
 OS Homo sapiens.
 XX Key Disulfide-bond Location/Qualifiers 1..6
 XX PN WO957149-A2.
 XX PD 11-NOV-1999.
 XX PF 05-MAY-1999; 99WO-CA000363.
 XX PF 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX PI Biaschuk OW, Gour BJ, Byers S;
 XX DR WPI; 2000-038791/03.
 XX PT New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX PS Claim 72: Page 193: 252pp; English.
 XX CC The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical-cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumor in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vaso permeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age -related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAY64572 represent specifically claimed peptides, and AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in the exemplification of the present invention
 XX SQ Sequence 6 AA;
 Query Match 65.8%; Score 25; DB 3; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 5
 AAY62006 standard; peptide; 6 AA.
 ID AAY62006
 XX AC AAY62006;
 DT 02-MAR-2000 (first entry)
 DE Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:1798.

RESULT 6
 AAY64259 standard; peptide: 6 AA.
 ID AAY64259;
 XX
 KW Modulation; nonclassical cadherin mediated cell adhesion recognition; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition; CAR;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3573.

OS Synthetic.
 OS Homo sapiens.
 XX Location/Qualifiers
 FH Key Daulfife-bond 1. .6
 FR XX
 PN WO957149-A2.
 PD XX
 PR 11-NOV-1999.
 PF 05-MAY-1999; 99WO-CA000363.
 XX
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 PA (ADHEREX) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Gour BJ, Byers S;
 XX
 DR WPI; 2000-038791/03.
 XX
 PT New cadherin modulating agents, used for modulating nonclassical cadherin
 -mediated functions for treating e.g. cancers, obesity, rheumatoid
 arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 PA Claim 4B: Page 180; 252pp; English.
 XX
 CC The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vaso permeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for e.g.
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age-
 CC related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY6092 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAY633183 to AAY633186 represent sequences used in
 CC the exemplification of the present invention
 XX Sequence 6 AA;
 SQ Query Match 65.8%; Score 25; DB 3; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 CYP LTC 6
 Db 1 CDPKTC 6

XX
 KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3573.

OS Synthetic.
 OS Homo sapiens.
 XX Location/Qualifiers
 FH Key Disulfide-bond 1. .6
 FT XX
 PN WO957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PP 05-MAY-1999; 99WO-CA000363.
 XX
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 PA (ADHEREX) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Gour BJ, Byers S;
 XX
 DR WPI; 2000-038791/03.
 XX
 PT New cadherin modulating agents, used for modulating nonclassical cadherin
 -mediated functions for treating e.g. cancers, obesity, rheumatoid
 arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 PA Claim 102; Page 217; 252pp; English.
 XX
 CC The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vaso permeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for e.g.
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age-
 CC related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY6092 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAY633183 to AAY633186 represent sequences used in
 CC the exemplification of the present invention
 XX

SQ	Sequence 6 AA;
Query Match	63.2% ; Score 24 ; DB 3 ; Length 6 ;
Best Local Similarity	50.0% ; Pred. No. 1.4e+06 ;
Matches 3 ; Conservative	2 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;
Qy	1 CVP LTC 6
Db	1 CDPVSC 6
RESULT 7	
ID	AY85373 standard; peptide; 6 AA.
XX	AY85373;
AC	AY85373;
XX	19-JUN-2000 (first entry)
XX	IL-2 derived anti-inflammatory peptide pep1.
DB	XX
KW	Interleukin-2; IL-2; antiinflammatory; antiarthritic; antirheumatic;
KW	antidiabetic; neuroprotective; dermatological; immunosuppressive;
KW	ophthalmological; autoimmune disease; multiple sclerosis; uveitis;
KW	systemic lupus erythematosus; Crohn's disease.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO20011038-A2.
XX	
PD	02-MAR-2000 .
XX	
PF	19-AUG-1999 ; 99WO-IL000448.
XX	
PR	21-AUG-1998 ; 98GB-00018370.
PR	31-AUG-1998 ; 98IL-00124009.
PR	16-MAY-1999 ; 99IL-00129980.
XX	
PA	(YEDA) YEDA RES & DEV CO LTD.
XX	
PI	Lider O, Arieli A, Herskovic R, Yavin EJ, Fridkin M;
XX	
DR	WPI; 2000-256367/22.
XX	
PT	Synthetic antiinflammatory peptide derived from IL-2 and its derivatives useful for treating inflammatory autoimmune diseases such as rheumatoid arthritis, multiple sclerosis and systemic lupus erythematosus.
PT	
PT	Claim 6 ; Page 35; 49pp; English.
XX	
CC	The invention provides synthetic antiinflammatory peptides derived from interleukin-2 (IL-2). They can be used for inhibition of adhesion of activated T-cells to ECM proteins such as fibronectin, laminin, collagen type-IV; inhibition of chemotactic migration of T-cell through RCM proteins preferably fibronectin; inhibition of cytokine or mitogen induced T-cell proliferation; inhibition of spontaneous or induced, preferably TNF-alpha induced cytokine secretion (e.g. IL-8, IL-beta) by stimulated T-cells and intestinal epithelial cells. The anti-inflammatory peptides and their derivatives are useful for preparing compositions for treating and/or alleviating chronic or acute inflammatory disorders and autoimmune diseases such as rheumatoid arthritis, diabetes type-I, multiple sclerosis, systemic lupus erythematosus, bowel inflammation, uveitis, and Crohn's disease. Sequences AAY85366-374 represent modified anti-inflammatory derivative peptides derived from the IL-2 derived anti-inflammatory peptide pep1 (AY85363).
CC	
CC	Sequence 6 AA;
XX	
SQ	Query Match 60.5% ; Score 23 ; DB 3 ; Length 6 ;
Best Local Similarity 50.0% ; Pred. No. 1.4e+06 ;	
Matches 3 ; Conservative 1 ; Mismatches 2 ; Indels 0 ; Gaps 0 ;	

RESULT 8	
Qy	1 CVPILTC 6 : 1 CIVLAC 6
ID	AY62757
AC	AY62757;
XX	
XX	02-MAR-2000 (first entry)
XX	PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4040.
DE	
KW	Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition;
KW	cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12
KW	cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW	cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW	desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW	rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW	neurological disease; cyclic.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Disulfide-bond 1..6
NN	PN WO957149-A2.
XX	PD 11-NOV-1999.
XX	PF 05-MAY-1999; 99WO-CA000363.
XX	PR 05-MAY-1998; 98US-00073040.
XX	PR 06-NOV-1998; 98US-00187859.
XX	PR 20-JAN-1999; 99US-00234395.
XX	PR 08-MAR-1999; 99US-00264516.
XX	PA (AHEE-) ADHEREX TECHNOLOGIES INC.
XX	Blaschuk OW, Gour BJ, Byers S;
PI	WPI; 2000-038791/03.
XX	
PT	New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
PT	Claim 72; Page 193; 252pp; English.
XX	
CC	The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical-cadherin expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vaso-activity in a mammal, enhancing adhesion of nonclassical-cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and in biofactors products can also be used for detection and diagnosis and in biofactors

CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY61643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX

Sequence 6 AA:

Query Match	60.5%	Score 23;	DB 3;	Length 6;
Best Local Similarity	66.7%	Pred. No.	1.4e+06;	
Matches	4;	Mismatches	2;	Indels 0;
QY	1 CVPITC 6			
Db	1 CDELTIC 6			

RESULT 9
 AAI62488 ID AAY62488 standard; peptide; 6 AA.
 XX
 AAI62488;
 AC
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE Cadherin-15 cell adhesion recognition cyclic peptide SEQ ID NO:2154.
 XX

KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX

Synthetic.
 OS Homo sapiens.
 XX
 FH Disulfide-bond 1..6
 XX
 PN WO957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA000363.
 XX
 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-0234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 PA (ADHES-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Gour BJ, Byers S;
 XX
 DR WPI; 2000-038791/03.

PT New cadherin modulating agents, used for modulating nonclassical cadherin
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoïd
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 PS Claim 60; Page 188; 252pp; English.
 XX
 PT The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating

CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vascular permeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age-
 CC related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY61643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX

Sequence 6 AA:

Query Match 60.5%; Score 23; DB 3; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CVPLTC 6
 Db 1 CDELTIC 6

RESULT 10

AAY44431

ID AAY44431 standard; peptide; 6 AA.

XX

AC AAY44431;

XX

DT 22-MAR-2000 (first entry)

XX

DE Peptide 1 derived from domain 1 of human beta-2 glycoprotein I.

XX

KW Human beta-2 glycoprotein I; beta-2 GPI; toleragen; B cell anergy;

KW beta-2 GPI-dependent antiphospholipid antibody; thrombosis;

KW recurrent foetal loss; thrombocytopenia; autoimmune disease;

KW systemic lupus erythematosus; coagulation assay.

XX

OS Homo sapiens.

XX

PN WO9964595-A1.

XX

PD 16-DBC-1999.

XX

PF 09-JUN-1999;

99WO-US013194.

XX

PR 09-JUN-1998;

98US-0088656P.

XX

PR 05-OCT-1998;

98US-0103088P.

XX

PR 08-JUN-1999;

99US-0028199.

XX

PA (LJOL-) LA JOLLA PHARM CO.

XX

PI Marquis DM, Iverson GM, Victoria EJ, Jones DS, Linnik MD;

XX

DR WPI; 2000-116542/10.

XX

New isolated domain 1 beta-2 GPI polypeptides, used for inhibiting

PT antiphospholipid antibodies for treating, e.g. thrombosis.

XX

PS Claim 3; Page 19; 158pp; English.

XX

The present sequence is a phospholipid binding serum protein. Isolated

CC domain 1 of beta-2 GPI protein binds to and inhibits beta-2 GPI-dependent

CC antiphospholipid antibodies. The fragments are useful as tolerogens when

CC they bind to the antibodies at the surface of a B cell and triggers B

CC cell anergy. The polypeptides and mimetics can be used for treating

CC disorders associated with beta-2 GPI-dependent GPI-associated pathologies,

CC e.g. thrombosis, recurrent foetal loss, thrombocytopenia or autoimmune

CC diseases such as systemic lupus erythematosus. The polypeptides can also

be used to detect and purify antibodies. They can also be used in

PR 20-NOV-1990; 90US-00615715.
 XX 16-JAN-1992; 92US-00822011.
 PA (TEXA) UNIV TEXAS .
 PX Reiss Y, Goldstein JL, Brown MS;
 XX DR WPI; 1995-206308/27.
 XX
 PR New farnesyl transferase inhibitor peptide(s) - based on farnesylation acceptor substrate carboxy terminal sequences, used for the treatment of cancer.
 XX
 PS Claim 2; Col 62; 55pp; English.
 XX
 CC AAR77800, AAR77805-R77838 are tetrapeptide inhibitors of farnesyl transferase. They all obey a generic formula for the C-terminal sequence of 4-10 amino acid inhibitory peptides; the formula is -C_nA_mX, where C= cysteine, A= any aliphatic, aromatic or hydroxy amino acid and X= any normal amino acid. Farnesyl transferase is involved in the farnesylation of various cellular proteins including the cancer related ras proteins. The transforming activity of ras is dependent on the localisation of the protein to membranes, a property which is thought to be dependent upon the addition of farnesyl groups. These peptide inhibitors are useful for treating cancers and ras-related cancers in particular. (Updated on 25-MAR-2003 to correct PCT field.)
 XX
 SQ Sequence 4 AA;

Query Match Score 22; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPL 4
 |||:
 Db 1 CVPM 4

RESULT 14
 AAW04459 ID AAW04459 standard; peptide; 4 AA.
 XX AC AAW04459;
 XX DT 30-JUL-1997 (first entry)
 XX
 PR 29-APR-1996; 96WO-US005969.
 XX PR 27-APR-1995; 95US-00429964.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Brown MS, Goldstein JL, James GL;
 XX DR WPI; 1996-497642/49.
 XX
 PT Assay for farnesyl transferase activity - by determining ability to transfer farnesyl moiety to K-Ras B protein, partic. useful for identifying inhibitors.
 XX
 Disclosure; Page 34; 257pp; English.

CC AAW04433-W04465 are peptide inhibitors of farnesyl transferase (PT activity. The peptides block the attachment of prenyl groups to ras proteins in malignant cells of patients suffering from cancer or a precancerous state and as such are used to treat cancer. The peptides were identified by determining the ability of candidate substances to inhibit a PT enzyme, by inhibiting the transfer of a farnesyl moiety to a K-RasB protein

XX
 SQ Sequence 4 AA;

Query Match Score 22; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPL 4
 |||:
 Db 1 CVPM 4

RESULT 15
 AAW67428 ID AAW67428 standard; peptide; 5 AA.
 XX
 AC AAW67428;
 XX DT 02-MAR-1999 (first entry)
 XX
 DE HCV peptide analogue #2.
 XX
 KW Hepatitis C virus; HCV; nucleocapsid; core protein; analogue; antibody; non-structural protein; thioamide bond; peptide bond.
 XX
 AC
 XX DT 02-MAR-1999 (first entry)
 XX
 DE HCV peptide analogue #2.
 XX
 KW Hepatitis C virus; HCV; nucleocapsid; core protein; analogue; antibody; non-structural protein; thioamide bond; peptide bond.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Modified-site 1 /note= "side chain protected by butyl group"
 FT Modified-site 2 /note= "side chain protected by butyl group"
 FT Modified-site 3 /note= "side chain protected by tosyl group"
 FT Disulfide-bond 5 /note= "side chain protected by benzoyl group and C-terminus protected by benzyl group"
 XX
 JP10226698-A.
 XX
 PD 25-AUG-1998.
 XX
 PR 19-FEB-1997; 97JP-00034702.
 XX
 PR 19-FEB-1997; 97JP-00034702.
 XX
 PA (KYOW) KYOWA MEDEX KK.
 XX
 DR WPI; 1998-515103/44.
 XX
 PT Determination of antibody in sample - uses peptide analog absorbed or chemically bound on carrier as antigen.
 XX
 PS Example 1; Page 9; 13pp; Japanese.

XX
 CC This sequence represents an analogue peptide of the Hepatitis C virus (HCV) nucleocapsid core protein. The invention relates to peptide analogues derived from HCV proteins, e.g. AAW67417-W67426, which can be used for the determination of anti-HCV antibodies in a sample. Preferably the peptide analogues contain one or more thioamide bonds where at least one oxygen atom of the peptide bond is replaced by sulphur atom. The peptide analogues can be adsorbed or chemically bound to a carrier

XX
 SQ Sequence 5 AA;

Query Match Score 22; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;

Sun Sep 5 11:41:03 2004

us-09-761-636a-12.closed.rag

Page 9

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Db	1	CRPLT	5							

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Job time : 64 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:26:47 ; Search time 67 Seconds

(without alignments)
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Perfect score: 38

Sequence: 1 CVPLTC 6

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Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 28303

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Maximum DB seq length: 6

Post-processing: Minimum Match 10%

Maximum Match 10%

Listing first 45 summaries

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18: /cgns_6/_ptodata/2/_pubpaas/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	26	68.4	6	14 US-10-006-869-1374	Sequence 1374, Appl
3	26	68.4	6	15 US-10-006-869-1374	Sequence 1374, Appl
4	25	65.8	6	14 US-10-006-869-1798	Sequence 1798, Appl
5	25	65.8	6	14 US-10-006-869-3970	Sequence 3970, Appl
6	25	65.8	6	14 US-10-006-869-4046	Sequence 4046, Appl
7	25	65.8	6	15 US-10-006-869-4046	Sequence 4046, Appl
8	25	65.8	6	15 US-10-006-869-4046	Sequence 4046, Appl
9	25	65.8	6	15 US-10-006-869-4046	Sequence 4046, Appl
10	25	65.8	6	16 US-10-006-869-4046	Sequence 4046, Appl
11	24	63.2	6	14 US-10-006-869-3573	Sequence 3573, Appl
12	24	63.2	6	15 US-10-006-869-3573	Sequence 3573, Appl
13	23	60.5	6	14 US-10-006-869-2154	Sequence 2154, Appl
14	23	60.5	6	14 US-10-006-869-4040	Sequence 4040, Appl
15	23	60.5	6	15 US-10-006-869-2154	Sequence 2154, Appl

RESULT 1
US-09-761-636A-12
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; STACKER, Steven
; HUGHES, Richard
; CENDRON, Angelia
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/45505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIORITY APPLICATION NUMBER: US 60/176,293
; PRIORITY FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-761-636A-12

RESULT 2
US-10-006-869-1374
; Sequence 1374, Appl
; Best Local Similarity 100.0%; Score 38; DB 9; Length 6;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 CVPLTC 6
; Db 1 CVPLTC 6
; Sequence 1374, Application US/10006869
; Publication No. US2003008216A1

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; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086_40/C7
; CURRENT APPLICATION NUMBER: US/10/006, 869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1374
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-006-869-1374

Query Match      68.4%;  Score 26;  DB 14;  Length 6;
Best Local Similarity 66.7%;  Pred. No. 1.2e+06;
Matches 4;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;
RESULT 3
US-10-395-032-1374
; Sequence 1374, Application US/10395032
; Publication No. US20030229199A1
GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086_40/C9
; CURRENT APPLICATION NUMBER: US/10/395, 032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1374
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-395-032-1374

Query Match      68.4%;  Score 26;  DB 15;  Length 6;
Best Local Similarity 66.7%;  Pred. No. 1.2e+06;
Matches 4;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;
RESULT 4
US-10-006-869-1798
; Sequence 1798, Application US/10006869
; Publication No. US20030082166A1
GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086_40/C7
; CURRENT APPLICATION NUMBER: US/10/006, 869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 4046
LENGTH: 6
TYPE: PRT

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ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative Cyclic modulating agent based on
 US-10-006-869-4046
 PB-cadherin cell adhesion recognition sequence

Query Match 65.8%; Score 25; DB 14; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;
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 SEQ ID NO 1798 LENGTH: 6

RESULT 9
 US-10-395-032-1798
 ; Sequence 1798, Application US/10395032
 ; Publication No. US20030229199A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; ATTORNEY OR AGENT NAME: Symonds, James Matthew
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL CADHERIN-MEDIATED FUNCTIONS
 ; CURRENT APPLICATION NUMBER: 1000B6 407C9
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
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 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
 ; SEQ ID NO 1798 LENGTH: 6

Query Match 65.8%; Score 25; DB 15; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;
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 SEQ ID NO 1798 LENGTH: 6

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 US-10-422-571-75
 ; Sequence 75, Application US/10422571
 ; Publication No. US2004008347A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Raitano, Arthur B.
 ; ATTORNEY OR AGENT NAME: Jakobovits, Ayia M.
 ; TITLE OF INVENTION: Entitled 191P4D12(b) Useful in Treatment and Detection of Cancer
 ; CURRENT APPLICATION NUMBER: 51158-2008-00
 ; CURRENT FILING DATE: 2003-04-23
 ; PRIOR APPLICATION NUMBER: US60/404,306
 ; PRIOR FILING DATE: 2002-08-16
 ; NUMBER OF SEQ ID NOS: 130
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 75
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

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Qy 3 PLTC 6
Db 3 PLTC 6

RESULT 11
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; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006, 869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3573
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor-cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-006-869-3573

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Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVPPLTC 6
Db 1 CDPVSC 6

RESULT 12
US-10-395-032-3573
; Sequence 3573, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395, 032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3573
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-395-032-3573

Query Match 63.2%; Score 24; DB 15; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVPPLTC 6
Db 1 CDPVSC 6

RESULT 13
US-10-006-869-2154
; Sequence 2154, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006, 869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2154
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence
US-10-006-869-2154

Query Match 60.5%; Score 23; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPPLTC 6
Db 1 CDEPLTC 6

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; Sequence 4040, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006, 869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-10-006-869-4040

Query Match 60.5%; Score 23; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPPLTC 6
Db 1 CDEPLTC 6

RESULT 15
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; Sequence 2154, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.

APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086_407C9
CURRENT APPLICATION NUMBER: US10/395,032
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SEQ ID NO: 2154
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
US-10-395-032-2154
OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence

Query Match 60.5%; Score 23; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPILTC 6
| | |
Db 1 CDELTIC 6

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Job time : 68 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 11:25:22 ; Search time 20 Seconds
 Perfect score: 38
 Sequence: 1 CVPJTC 6

Title: US-09-761-636A-12

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Post-processing: Minimum Match 0%
 Maximum Match 100%
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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	68.4	6	4 US-09-187-859-1374	Sequence 1374, AP
2	26	68.4	6	4 US-09-839-542B-1374	Sequence 1374, AP
3	25	65.8	6	4 US-09-187-859-1798	Sequence 1798, AP
4	25	65.8	6	4 US-09-187-859-3970	Sequence 3970, AP
5	25	65.8	6	4 US-09-187-859-4046	Sequence 4046, AP
6	25	65.8	6	4 US-09-839-542B-1798	Sequence 1798, AP
7	25	65.8	6	4 US-09-839-542B-3970	Sequence 3970, AP
8	25	65.8	6	4 US-09-839-542B-4046	Sequence 4046, AP
9	24	63.2	6	4 US-09-187-859-3573	Sequence 3573, AP
10	24	63.2	6	4 US-09-839-542B-3573	Sequence 3573, AP
11	23	60.5	6	4 US-09-187-859-2154	Sequence 2154, AP
12	23	60.5	6	4 US-09-187-859-4040	Sequence 4040, AP
13	23	60.5	6	4 US-09-839-542B-2154	Sequence 2154, AP
14	23	60.5	6	4 US-09-839-542B-4040	Sequence 4040, AP
15	22	57.9	4	2 US-08-429-964-41	Sequence 41, APPL
16	22	57.9	4	5 PCT-US93-08062-41	Sequence 41, APPL
17	22	57.9	4	5 PCT-US93-08062-35	Sequence 41, APPL
18	22	57.9	6	4 US-09-187-859-1737	Sequence 1737, AP
19	22	57.9	6	4 US-09-187-859-2719	Sequence 2719, AP
20	22	57.9	6	4 US-09-839-542B-1737	Sequence 1737, AP
21	22	57.9	6	4 US-09-839-542B-2719	Sequence 2719, AP
22	21	55.3	5	4 US-09-082-358B-90	Sequence 90, APPL
23	21	55.3	5	4 US-09-050-861B-24	Sequence 24, APPL
24	21	55.3	6	4 US-09-187-859-1885	Sequence 1885, AP
25	21	55.3	6	4 US-09-187-859-2747	Sequence 2747, AP
26	21	55.3	6	4 US-09-839-542B-1885	Sequence 1885, AP
27	21	55.3	6	4 US-09-839-542B-2747	Sequence 2747, AP

ALIGNMENTS

RESULT 1
 US-09-187-859-1374
 ; Sequence 1374, Application US/09187859A
 ; Parent No. 6358920
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 ; FILE REFERENCE: 100086 407C1
 ; CURRENT APPLICATION NUMBER: US/09-187, 859A
 ; CURRENT FILING DATE: 1998-11-06
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1374
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; US-09-187-859-1374

Query Match Similarity 68.4%; Score 26; DB 4; Length 6;
 Best Local Similarity 66.7%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 2; Indexes 0; Gaps 0;

Oy 1 CVPJTC 6
 Db 1 CEBKTC 6

RESULT 2
 US-09-839-542B-1374
 ; Sequence 1374, Application US/09839542B
 ; Parent No. 6556996
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Symonds, James Matthew
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 ; FILE REFERENCE: 100086 407D1
 ; CURRENT APPLICATION NUMBER: US/09/839, 542B
 ; CURRENT FILING DATE: 2001-04-20
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1374
 ; LENGTH: 6
 ; TYPE: PRT

i ORGANISM: Artificial Sequence
i FEATURE:
i OTHER INFORMATION: Representative cyclic modulating agent based on
i OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
i US-09-839-542B-1374

Query Match Score 26; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPJTC 6
Db 1 CDPKTC 6

RESULT 3
US-09-187-859-1798
Sequence 1798, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086_407C1
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SEQ ID NO: 1798
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
i US-09-187-859-1798

Query Match Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPJTC 6
Db 1 CDPKTC 6

RESULT 5
US-09-187-859-4046
Sequence 4046, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086_407C1
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SEQ ID NO: 4046
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
i US-09-187-859-4046

Query Match Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPJTC 6
Db 1 CDPKTC 6

RESULT 6
US-09-839-542B-1798
Sequence 1798, Application US/09839542B
Patent No. 6569396
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086_407D1
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SEQ ID NO: 1798
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
i US-09-839-542B-1798

Query Match Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPJTC 6
Db 1 CDPKTC 6

RESULT 7
US-09-839-542B-3970
Sequence 3970, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086_407C1
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SEQ ID NO: 3970
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
i US-09-187-859-3970

Query Match Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Sequence 3970, Application US/09839542B
 GENERAL INFORMATION:
 APPLICANT: Blaschuk, Orest W.
 APPLICANT: Symonds, James Matthew
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 FILE REFERENCE: 100086.407C1
 CURRENT APPLICATION NUMBER: US/09/187,859A
 CURRENT FILING DATE: 1998-11-06
 NUMBER OF SEQ ID NOS: 4052
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 3970
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative cyclic modulating agent based on
 OTHER INFORMATION: Cadherin-related neuronal receptor cell adhesion
 SEQ ID NO 3970

Query Match 65.8%; Score 25; DB 4; Length 6;
 Best Local Similarity 66.7%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CVPPLTC 6
 Db 1 CDPVSC 6

RESULT 10
 US-09-839-542B-3573
 ; Sequence 3573, Application US/09839542B
 ; Patent No. 6569956
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Symonds, James Matthew
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; FILE REFERENCE: 100086.407D1
 ; CURRENT APPLICATION NUMBER: US/09/839,542B
 ; CURRENT FILING DATE: 2001-04-20
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3573
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Representative cyclic modulating agent based on
 ; OTHER INFORMATION: Cadherin-related neuronal receptor cell adhesion
 ; OTHER INFORMATION: recognition sequence
 ; SEQ ID NO-839-542B-3573

Query Match 63.2%; Score 24; DB 4; Length 6;
 Best Local Similarity 50.0%; Pred. No. 3e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CVPPLTC 6
 Db 1 CDPVSC 6

RESULT 11
 US-09-187-859-2154
 ; Sequence 2154, Application US/09187859A
 ; Patent No. 6339920
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; FILE REFERENCE: 100086.407C1
 ; CURRENT APPLICATION NUMBER: US/09/187,859A
 ; CURRENT FILING DATE: 1998-11-06
 ; NUMBER OF SEQ ID NOS: 4052
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2154

RESULT 9
 US-09-187-859-3573
 ; Sequence 3573, Application US/09187859A
 ; Patent No. 6339920
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaschuk, Orest W.
 ; APPLICANT: Gour, Barbara J.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative cyclic modulating agent based on
 OTHER INFORMATION: Cadherin-15 cell adhesion recognition sequence
 US-09-187-859-2154

Query Match 60.5%; Score 23; DB 4; Length 6;
 Best Local Similarity 66.7%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVP LTC 6
 Db 1 CDEL LTC 6

RESULT 12
 US-09-187-859-4040
 Sequence 4040, Application US/09187859A
 Patent No. 6358920
 GENERAL INFORMATION:
 APPLICANT: Blaschuk, Orest W.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 FILE REFERENCE: 100086.407D1
 CURRENT APPLICATION NUMBER: US/09/187,859A
 CURRENT FILING DATE: 1998-11-06
 NUMBER OF SEQ ID NOS: 4052
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 4040
 LENGTH: 6

TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative cyclic modulating agent based on
 OTHER INFORMATION: Cadherin-15 cell adhesion recognition sequence
 US-09-187-859-4040

Query Match 60.5%; Score 23; DB 4; Length 6;
 Best Local Similarity 66.7%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVP LTC 6
 Db 1 CDEL LTC 6

RESULT 13
 US-09-839-542B-2154
 Sequence 2154, Application US/09839542B
 Patent No. 6569986
 GENERAL INFORMATION:
 APPLICANT: Blaschuk, Orest W.
 APPLICANT: Symonds, James Matthew
 APPLICANT: Gour, Barbara J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 FILE REFERENCE: 100086.407D1
 CURRENT APPLICATION NUMBER: US/09/839,542B
 CURRENT FILING DATE: 2001-04-20
 NUMBER OF SEQ ID NOS: 4052
 LENGTH: 6

TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative cyclic modulating agent based on
 OTHER INFORMATION: Cadherin-15 cell adhesion recognition sequence
 US-09-839-542B-2154

Query Match 60.5%; Score 23; DB 4; Length 6;
 Best Local Similarity 66.7%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVP LTC 6
 Db 1 CDEL LTC 6

RESULT 14
 US-09-839-542B-4040
 Sequence 4040, Application US/09839542B
 Patent No. 6569986
 GENERAL INFORMATION:
 APPLICANT: Blaschuk, Orest W.
 APPLICANT: Symonds, James Matthew
 APPLICANT: Gour, Barbara J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 FILE REFERENCE: 100086.407D1
 CURRENT APPLICATION NUMBER: US/09/839,542B
 CURRENT FILING DATE: 2001-04-20
 NUMBER OF SEQ ID NOS: 4052
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 4040
 LENGTH: 6

TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative cyclic modulating agent based on
 OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
 US-09-839-542B-4040

Query Match 60.5%; Score 23; DB 4; Length 6;
 Best Local Similarity 66.7%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVP LTC 6
 Db 1 CDEL LTC 6

RESULT 15
 US-09-839-964-41
 Sequence 41, Application US/09429964
 Patent No. 5962243
 GENERAL INFORMATION:
 APPLICANT: BROWN, MICHAEL S.
 APPLICANT: GOLDSTEIN, JOSEPH L.
 APPLICANT: REISS, YUVAL
 APPLICANT: JAMES, GUY L.
 TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
 TITLE OF INVENTION: TRANSFERASE INHIBITORS
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ARNOLD, WHITE & DURKEE
 STREET: P.O. BOX 4433
 CITY: HOUSTON
 STATE: TEXAS
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/429,964
 FILING DATE: 27-APR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/021,625
 FILING DATE: 16-FEB-1993

CLASSIFICATION: 435
APPLICATION NUMBER: US 07/822,011
FILING DATE: ABANDONED
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US/91/02650
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:432/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-429-964-41

Query Match Score 22; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 3e-05; Mismatches 0; Gaps 0;
Matches 3; Conservative 1; Indels 0;

QY	1	CYPL	4
		:	
Db	1	CVPM	4

Search completed: September 5, 2004, 11:30:16
Job time : 21 secs

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Run on:	September 5, 2004, 11:31:03 ; Search time 23 Seconds (without alignments)	Total number of hits satisfying chosen parameters: 1101	RESULT 1
Minimum DB seq length:	0	Query	165546
Maximum DB seq length:	10	Match	MHC H2-L antigen - mouse (fragment)
Post-processing:	Maximum Match 0% Listing First 45 summaries	Score	C;Species: Mus musculus (house mouse)
Database :	PIR 78: 1: p1r1: 2: p1r2: 3: p1r3: 4: p1r4: A;Accession: I65546 A;Status: Preliminary; translated from GB/EMBL/DBJ/	Length	C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
		DB	C;Accession: I65546 R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P. Cell 44, 261-272, 1986 A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their relationship to the H-2Kb gene A;Reference number: I52778; MUID:8610622; PMID:3510743
		Indels	A;Residues: 1-6 <RES> A;Cross-references: GB:MI2483; NID:9199565; PIDN:AAA39663.1; PID:9554234
		Gaps	
		0;	
Searched:	283366 seqs, 96191526 residues	Best Local Similarity	35.7%; Score 20; DB 2; Length 6;
		Matches	C;Alternates: Liiza ramada
		3;	R;Bonamusa, L.; Baanante, J.V. Comp. Biochem. Physiol. B 95, 295-301, 1990 A;Title: Purification and characterization of glycogen phosphorylase b A;Reference number: A60521; MUID: 90227907; PMID:209669
		Conservative	A;Accession: A60521 A;Molecule type: protein A;Residues: 1-5 <BON>
		0;	C;Superfamily: Glucan phosphorylase C;Keywords: Glycosyltransferase; hexosyltransferase; phosphoprotein F;3/Binding site: phosphate (ser) (covalent) (by phosphorylase b kinase) #status experiment
		Mismatches	
		0;	
Result No.	Score	Query	8 VPC 10
		Match	Qy
		Length	Db
		ID	VPC
		Description	4
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1	20	35.7	165546
2	19	33.9	MHC H2-L antigen -
3	19	33.9	glycogen phosphorylase
4	18	32.1	Ig heavy chain CR
5	17	30.4	Ig heavy chain CRD
6	17	30.4	vitellogenin, 190k
7	16	28.6	T-cell receptor beta
8	16	28.6	metallothionein-A
9	16	28.6	205k exoantigen -
10	16	28.6	polygalacturonase
11	15	26.8	T-cell receptor beta
12	15	26.8	major postsynaptic
13	15	26.8	ATP-binding protein
14	15	26.8	cytochrome-C oxidase
15	14	25.0	hypothetical protein
16	14	25.0	polycoeruloplasmin
17	14	25.0	myomodulin - Calif
18	14	25.0	gene Ctfar protein
19	14	25.0	118k stomach cancer
20	14	25.0	collagen alpha 2(VI)
21	14	25.0	amicanin - Paraco
22	14	25.0	sphingomyelinase -
23	14	25.0	protein P7 - curle
24	14	25.0	aryl hydrocarbon (
25	14	25.0	alpha-Gliadin 4Ha
26	14	25.0	alpha-Gliadin 6Ha
27	13	23.2	Na+/K+-exchanging
28	13	23.2	flagellar protein
29	13	23.2	conopressin S - co
		9	cytochrome-c oxidase

RESULT 3
C39111 Ig heavy chain C region - Pacific hagfish (fragment)
C;Species: *Eptatretus stouti* (Pacific hagfish)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
R;Varner, J.; Neame, P.J. Litman, G.W.
A;Title: A serum heterodimer from hagfish (*Eptatretus stoutii*) exhibits structural similarity to the rat v-D-J region (clone 15) - rat (fragment)
A;Reference number: A39111; MUID:91156684; PMID:200362
A;Accession: C39111
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 1-10 <VAR>
C;Keywords: heterotetramer; immunoglobulin

Query Match Score 19; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ISVPLSV 8
Db 4 ISSPLVV 10

RESULT 4
PT0247 Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and junctional diversity in the rainbow trout (Oncorhynchus mykiss) membrane
A;Reference number: PT0222; MUID:91108337; PMID:189102
A;Accession: PT0247
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match Score 18; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 SVPSVVP 9
Db 2 SAPIDSP 8

RESULT 5
A6122 vitellogenin, 190k chain - gypsy moth (fragment)
N;Contains: vitellin
C;Species: Lymantria dispar (gypsy moth)
C;Accession: A6122
R;Hiremath, S.; Bhatia, S.
Insect Biochem. Mol. Biol. 22, 605-611, 1992
A;Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantria dispar
A;Reference number: A61622
A;Accession: A61622
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <HIR>
C;Keywords: egg yolk; hemolymph

Query Match Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PLSVVP 9
||:

Db 2 PLTEP 6

RESULT 6
PH0944 T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C;Species: *Rattus norvegicus* (Norway rat)
C;Accession: PH0944
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T-cell receptor beta chains in Lewis rats with experimental allergic encephalitis
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0944
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
A;Note: the authors translated the codon GAC for residue 9 as Glu
C;Keywords: T-cell receptor

Query Match Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CISVYP 5
Db 1 CASSVP 5

RESULT 7
IS1049 metallothionein-A - rainbow trout (rainbow trout)
C;Species: *Oncorhynchus mykiss* (rainbow trout)
C;Accession: IS1049
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: IS1049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) metallothionein-A
A;Accession: IS1049; MUID:95324545; PMID:7601121
A;Accession: IS1049
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <OLS>
A;Cross-references: EMBL:X00181; NID:91019799; PID:CAA5666..1; PID:94379328

Query Match Score 16; DB 2; Length 4;
Best Local Similarity 10.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PC 10
Db 3 PC 4

RESULT 8
G33098 20S exoantigen - malaria parasite (Plasmodium falciparum) (fragment)
C;Species: Plasmodium falciparum
C;Accession: G33098
R;Nicholls, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Accession: G33098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <NIC>
A;Accession: G33098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <NIC>

Query Match Score 16; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VPLSV 8

RESULT 9
 Db : 2 VPLXL 6 Qy : 6 LSVP 9
 Db : 2 LXVP 5

RESULT 10
 S62880 polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
 C;Species: Aspergillus sp.
 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C;Accession: S62880
 R;Stratilova, E.; Dzurova, M.; Markovic, O.; Joernvall, H.
 FEBS Lett. 382, 164-166, 1996
 A;Title: An essential tyrosine residue of Aspergillus polygalacturonase.
 A;Reference number: S62880; PMID:8612742
 A;Accession: S62880
 A;Molecule type: protein
 A;Residues: 1-10 <STR>
 C;Keywords: glycosidase; hydrolase
 F;4/Active site: Tyr #status predicted

Query Match	28.6%	Score 16;	DB 2;	Length 10;
Best Local Similarity	100.0%	Pred. No. 7.2e+03;		
Matches	2;	Conservative 0;	Mismatches 0;	Indels 0;
Qy	9 PC 10			
Db	9 PC 10			

Query Match 28.6% | Score 16; | DB 2; | Length 10; |

Best Local Similarity 100.0% | Pred. No. 7.2e+03; | | |

Matches 2; | Conservative 0; | Mismatches 0; | Indels 0; |

Qy

Db

RESULT 11
 A426B9 major postsynaptic density protein - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 26-May-1994
 C;Accession: A426B9
 R;Wu, K.; Hung, Y.; Adler, J.; Black, I.B.
 Proc. Natl. Acad. Sci. U.S.A. 89, 3015-3019, 1992
 A;Title: On the identity of the major postsynaptic density protein.
 A;Reference number: A426B9; PMID:1313576
 A;Accession: A426B9
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-8 <WUA>

Query Match	26.8%	Score 15;	DB 2;	Length 8;
Best Local Similarity	75.0%	Pred. No. 2.8e+05;		
Matches	3;	Conservative 0;	Mismatches 1;	Indels 0;
Qy				
Db				

RESULT 12
 A49712 ATP-binding protein p46 - dog (fragment)
 C;Species: Canis lupus familiaris (dog)
 C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
 C;Accession: B49712
 R;Nigam, S.K.; Goldberg, A.L.; Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.
 J. Biol. Chem. 269, 1744-1749, 1994
 A;Title: A set of endoplasmic reticulum proteins possessing properties of molecular chaperones.
 A;Reference number: A49712; PMID:94124514; PMID:8294423
 A;Accession: B49712
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <NIG>
 C;Keywords: ATP; endoplasmic reticulum; molecular chaperone

Query Match	26.8%	Score 15;	DB 2;	Length 9;
Best Local Similarity	33.3%	Pred. No. 2.8e+05;		
Matches	2;	Conservative 1;	Mismatches 3;	Indels 0;
Qy	4 VPLSVP 9			
Db	1 IPXXYP 6			

RESULT 13
 S43630 cytochrome-c oxidase (EC 1.9.3.1) chain VIC, hepatic - rainbow trout (fragment)
 C;Species: Oncorhynchus mykiss (rainbow trout)
 C;Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
 C;Accession: S43630
 R;Freund, R.; Kadenbach, B.
 Eur. J. Biochem. 221, 1111-1116, 1994
 A;Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome-c oxidase
 A;Accession number: S43624; PMID:94237150; PMID:8181469
 A;Accession: S43630
 A;Molecule type: protein
 A;Residues: 1-10 <FRB>
 A;Note: the source is designated as *Salmo gairdneri*
 C;Genetics:
 A;Genome: nuclear
 C;Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

Query Match	26.8%	Score 15;	DB 2;	Length 10;
Best Local Similarity	75.0%	Pred. No. 1.1e+04;		
Matches	3;	Conservative 0;	Mismatches 1;	Indels 0;
Qy	6 LSVP 9			
Db	2 LXVP 5			

RESULT 14
 B86128 hypothetical protein Z5903 [imported] - Escherichia coli (strain O157:H7, substrate EDL93)
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C;Accession: B86128
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, P.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamitis, K.; Apodaca, N.; Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; PMID:21074935; PMID:1206551
 A;Accession: B86128
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-10 <STO>

A;Cross-references: GB:AB005174; NID:912519314; PIDN:AAG59489_1; GSPDB:GN00145; UNGP:259
A;Experimental source: strain O157:H7, substrain EDL33
C;Genetics:
A;Gene: 25903

Query Match	26.8%	Score 15;	DB 2;	Length 10;
Best Local Similarity	60.0%	Pred. No.	1.1e+04;	
Matches	3;	Conservative	0;	Mismatches + 2;
				Indels 0;
QY	6 LSVP	C 10		Gaps 0;
Db	5 LQvvC	9		

RESULT 15

B22565 R-phycoerythrin alpha-2 chain - red alga (*Gastroclonium coulteri*) (fragment)C;Species: *Gastroclonium coulteri*

C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C;Accession: B22565

R;Klotz, A.V.; Glaser, A.N.

J. Biol. Chem. 260: 4856-4863, 1985

A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A;Reference number: A22565; MUID:85182601; PMID:3886644

A;Accession: B22565

A;Molecule type: protein

A;Residues: 1-5 <XLO>

Query Match	25.0%	Score 14;	DB 2;	Length 5;
Best Local Similarity	75.0%	Pred. No.	2.8e+05;	
Matches	3;	Conservative	0;	Mismatches + 1;
				Indels 0;
QY	6 LSVP	9		Gaps 0;
Db	1 LCV	4		

Search completed: September 5, 2004, 11:35:13

Job time : 23 secs

Scoring table:	BLOSUM62	RESULT 1
Gapop 10.0 , Gapext 0.5	MGMT_BOVIN	MGMT_BOVIN
Searched:	141681 seqs, 52070155 residues	ID MGMT_BOVIN STANDARD; PRT; 9 AA.
Total number of hits satisfying chosen parameters:	371	AC P29177; DT 01-DEC-1992 (Rel. 24, Created)
Minimum DB seq length: 0		DT 01-DEC-1992 (Rel. 24, Last sequence update)
Maximum DB seq length: 10		DT 01-OCT-1996 (Rel. 34, Last annotation update)
Post-processing: Minimum Match 0%		DE Methylated-DNA->protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methyl- <i>l</i> -guanine-DNA methyltransferase) (Fragment).
Maximum Match 100%		GN MGMT.
Listing First 45 summaries		OS Bos taurus (Bovine).
Database :	SwissProt_42:*	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.
		OC NCBI_TaxID=9913; OX [1]; RN
		RP SEQUENCE.
		RX TISSUE-thymus; RC MEDLINE=90174912; PubMed=2308822;
		RA Rydberg B.; Hall J.; Karran P.;
		"Active site amino acid sequence of the bovine 6-O-methylguanine-DNA methyltransferase."
		RL Nucleic Acids Res. 18:17-21(1990).
		CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the O-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is irreversibly inactivated.
		CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein S-methyl-L-cysteine.
		CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
		CC DR InterPro; IPR01497; Methytransferf_1.
		DR PROSITE; PS00374; MGMT; PARTIAL.
		KW DNA repair; Transferase; Methyltransferase.
		FT ACT_NTER 1 1 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
		FT ACT_SITE 9 9
		FT NON_NTER 9 9
		SEQUENCE 9 AA; 967 MW; 325171AT20476047 CRC64;
		Query Match 46.4% ; Score 26; DB 1, Length 9;
		Best Local Similarity 42.9%; Pred. No. 1.4e+05;
		Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
		Qy 4 VPLSVPCT 10
		Db 3 IPILTPC 9
		RESULT 2
		ID LPK2_LOCMI
		LPK2 LOCMI STANDARD; PRT; 10 AA.
		AC P41458;
		DT 01-NOV-1995 (Rel. 32, Created)
		DT 01-NOV-1995 (Rel. 32, Last sequence update)
		DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).
 OC Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea; Acrideridae; Locusta.
 OC NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE=Brain;
 RX MEDLINE=4094339; PubMed=7903606;
 RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
 de Loof A.; "Isolation, identification and synthesis of locustapyrokinin II from
 Locusta migratoria, another member of the FXPRL-amide peptide family",
 Comp. Biochem. Physiol. 106C:103-109 (1993).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 activity).
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro: IPR00148; Pyrokinin.
 PROTEIN: PS00539; PYROKININ: 1.
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidine carboxylic acid.
 FT MOD RES 1 1 PYRROLIDINE CARBOXYLIC ACID.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1145 MW; CFAF4221A9D1B772 CRC64;
 Query Match 33.9%; Score 19; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 8.8e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 SVPLSVP 9
 Db 2 SVPTTP 8

RESULT 3
 COW2_CONPU CO2_CONPU STANDARD; PRT; 8 AA.
 AC P58785;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leu-contryptphan-P.
 OS Conus purpurascens (Purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OC NCBI_TaxID=41690;

RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMTRY.
 RC STRAIN=Clipperton Island; TISSUE=Venom;
 RX MEDLINE=93388339; PubMed=10461743;
 RA Jacobson R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
 Oliveira B.M.; "A novel D-leucine-containing Conus peptide: diverse conformational
 dynamics in the contryphan family.", J. Pept. Res. 54:93-99(1999).
 RT DISULFID 2 8 D-LEUCINE.
 FT MOD RES 4 4 D-LEUCINE.
 SQ SEQUENCE 8 AA; 890 MW; 75A36767273CEB8 CRC64;

Query Match 32.1%; Score 18; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.4e-05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 4
 COXH_ONCMY STANDARD; PRT; 10 AA.
 AC P80331;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DB Cytochrome c oxidase polypeptide VIC (BC 1.9.3.1) (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo Gairdneri).
 OC Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Telostei; Euteleostei;
 OC Proracanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OC NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=liver;
 RX MEDLINE=94237150; PubMed=8181469;
 RA Freund R., Kadenbach B.;
 RT "Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout.";
 RL Eur. J. Biochem. 221:111-116 (1994).
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 DR PIR: S43630; S43630.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 977 MW; E11B40769DC772DA CRC64;

Query Match 26.8%; Score 15; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LSVP 9
 Db 2 LxVp 5

RESULT 5
 NS1_MYCTU STANDARD; PRT; 10 AA.
 AC P81135;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB 30 kDa non-secretory protein 1 (Fragment).
 OS Mycobacterium tuberculosis.
 OC Actinobacteria; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=H37Rv;
 RA Praasad H.K., Annapurna P.S.;
 RL Submitted (DEC-1997) to Swiss-Prot.
 CC -!- CAUTION: We are unable to find this protein in the translation of the genome of strain H37Rv.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;

Query Match 26.8%; Score 15; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 4.5e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISVPLSVP 9
 Db 1 :|||
 Db 1 MATPLVDP 8

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Brain.
 CC -!- METHOD=MALDI.
 CC -!- SIMILARITY: MW=1080.7; TACHYKININS.
 CC Tachykinin; Neuropeptides; Amidation.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1068 MW; C4541679C9C865BD CRC64;
 Query Match 25.0%; Score 14; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 VPLS 7
 Db 1 VPLS 4

RESULT 1.0
 E101_LITRU STANDARD PRT; 6 AA.
 AC P82096;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Electrin 1.
 OS Litoria rubella (Desert tree frog).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachii; Anura; Neobatrachia; Hylidae;
 OC Pelodryadinae; Litoria;
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE; Skin secretion;
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 Litoria electrica. Comparison with the skin peptides from Litoria
 rubella.";
 RT Aust. J. Chem. 52:639-645 (1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC Amphibian defense peptide; Amidation.
 FT MOD RES 6 6 AMIDATION.
 SQ SEQUENCE 6 AA; 792 MW; 6683704772CPA000 CRC64;

Query Match 23.2%; Score 13; DB 1; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VPL 6
 Db 2 VPL 4

RESULT 1.1
 CONO CONST STANDARD PRT; 9 AA.
 AC P05187;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Arg-conopressin S.
 OS Conus striatus (Striated cone).
 OC Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6493;
 RN [1]
 RP SEQUENCE;
 RX MEDLINE=88058932; PubMed=3680228;
 RX Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
 RA Gray W.R., Olivera B.M.;
 RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
 peptides from Conus geographus and Conus straitus venoms.";

RL J. Biol. Chem. 262:15821-15824 (1987).
 RN [2]
 RP REVIEW.
 RX MEDLINE=89024586; PubMed=305286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide Toxins from venomous Conus snails.";
 RL Ann. Rev. Biochem. 57:1665-700 (1988).
 CC -!- FUNCTION: Targets vasopressin/oxytocin related receptors.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
 DR PIR; B28495; B28495.
 DR InterPro; IPR000981; Neuhrhyp_horn.
 DR Pfam; PF00220; hormone4_1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6 AMIDATION.
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB540050 CRC64;
 Query Match 23.2%; Score 13; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CT 2
 Db 1 CT 2

RESULT 1.2
 COXE THIOB STANDARD PRT; 9 AA.
 ID COXE THIOB
 AC P8975;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIA (EC 1.9.3.1) (Fragment).
 OS Thunnus obesus (Bigeye tuna).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxID=8541;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=heart;
 RX MEDLINE=97451291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 liver.";
 RL Eur. J. Biochem. 248:99-103 (1997).
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
 chains of cytochrome c oxidase, the terminal oxidase in
 mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferricytochrome
 C + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase via family.
 DR PIR; S77984; S77984.
 DR InterPro; IPR001349; COX6A.
 DR PROSITE; PS01329; COX6A; PARTIAL.
 KW Oxidoreductase; inner membrane; Mitochondrion.
 FT NON TER 1 1
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;
 Query Match 23.2%; Score 13; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 PLSYP 9
 |||

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Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6	Q8aum7 carassius a
OM protein - protein search, using sw model		Q8spn8 macaca mula
Run on: September 5, 2004, 11:30:23 ; Search time 57 Seconds	(without alignments)	Q8saz9 pyrrhobryum
Title: US-09-761-636A-13	55.354 Million cell updates/sec	Q94is6 Pinus taeda
Perfect score: 56		Q42564 fagus rubrip
Sequence: 1 CISVPLSVPFC 10		Q915w6 liberibacteriae
Scoring table: BLOSUM62		Q8x4e5 escherichia
Gapext 10.0 , Gapext 0.5		Q07624 rous sarcoma
Searched: 1017041 seqs, 315518202 residues		Q9fxk1 prochlorococcus
Total number of hits satisfying chosen parameters: 1443		P72345 pseudomonas
Minimum DB seq length: 0		Q9k4m6 staphylococcus
Maximum DB seq length: 10		Q9ucs8 homo sapiens
Post-processing: Maximum Match 0% Listing First 45 summaries		Q9twv0 antiphleura
Database : SPTREMBL_25:*		Q9fxl0 lithium long
1: sp_archaea:*		Q9h3r9 homo sapiens
2: sp_bacteria:*		Q9h121 homo sapiens
3: sp_fungi:*		Q8maz9 dicranostyl
4: sp_human:*		Q8mbb7 merremia ae
5: sp_invertebrate:*		Q8s154 aconitum haematoxylum
6: sp_mammal:*		P83091 spinacia ol
7: sp_mhc:*		Q90347 hepatitis g
8: sp_organelle:*		Q8jv78 polyomavirus
9: sp_phage:*		Q9pru1 cynops pyrrhuloxanthus
10: sp_plant:*		Q87113 influenzae
11: sp_rabbit:*		Q8pkp4 microcytosis
12: sp_virus:*		Q94534 mycoplasma pneumoniae
13: sp_vertebrate:*		Q32560 escherichia coli
14: sp_unclassified:*		Q8iubb8 homo sapiens
15: sp_virus:*		Q8wf55 diadema paleaceum
16: sp_bacterioplasm:*		
17: sp_archeap:*		
ALIGNMENTS		
RESULT 1		
5: ID 035953; PRELIMINARY;		PRT; 9 AA.
AC 035953; DT 01-JAN-1998 (TREMBLrel. 05, Created)		
SP 035953; DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)		
PP 035953; DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
OB 035953; DE Truncated voltage-gated sodium channel alpha subunit (Fragment).		
GN SCNBA.		
OS Mus musculus (Mouse); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.		
OC NCBI_TAXID=10090; RN [1] _		
RP SEQUENCE FROM N.A.		
RC STRAIN=RITI;		
RX MEDLINE=97442476; PubMed=9295353;		
RA Plummer N.W., McBurney M.W., Meissler M.H.;		
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells."		
RL J. Biol. Chem. 272:24008-24015(1997).		
DR MGI:103165; Scnba.		
DR GO:0007628; P:adult walking behavior; IMP.		
KW Ionic channel		
RT NON_TER 1		
FT SQ SEQUENCE 9 AM; 898 MW;		22D92865B735BB737 CRC64;
Query Match 35.7%; Score 20; DB 11; Length 9;		
Best Local Similarity 80.0%; Pred. No. 1e+06;		
Matches 1; Mismatches 0; Indels 0; Gaps 0;		
Y Q 4 VPLSV 8		
7 17 30.4 8 4 Q94X6		
8 17 30.4 9 10 Q7X6A3		
9 17 30.4 10 8 Q96041		
10 17 30.4 10 10 Q7Y018		
11 17 30.4 10 12 Q956140		
12 16 28.6 8 4 Q15898		
13 16 28.6 8 6 Q02831		
14 16 28.6 8 6 Q9TRY3		
15 16 28.6 9 12 Q8QVD3		
16 16 28.6 9 13 Q8AYL5		
SUMMARIES		
Result No. Score Query Match Length DB ID Description		
1 20 35.7 9 11 035953		O35953 mus musculus
2 20 35.7 10 15 085598		Q85598 moloney murine leukaemia virus
3 20 35.7 10 15 085563		Q85563 moloney murine leukaemia virus
4 20 35.7 10 15 085619		Q85619 moloney murine leukaemia virus
5 19 33.9 8 2 Q56140		Q56140 streptococcus
6 19 33.9 10 2 Q7WUG2		Q7wug2 escherichia coli
7 17 30.4 8 4 Q94X6		Q94X6 homo sapiens
8 17 30.4 9 10 Q7X6A3		Q7x6a3 zea mays subsp. mays
9 17 30.4 10 8 Q96041		Q96041 oenothera lamarckiana
10 17 30.4 10 10 Q7Y018		Q7Y018 zea mays subsp. mays
11 17 30.4 10 12 Q956140		Q956140 hepatitis B virus
12 16 28.6 8 4 Q15898		Q15898 homo sapiens
13 16 28.6 8 6 Q02831		Q02831 oryctolagus cuniculus
14 16 28.6 8 6 Q9TRY3		Q9TRY3 sus scrofa
15 16 28.6 9 12 Q8QVD3		Q8QVD3 ovine respiratory syncytial virus
16 16 28.6 9 13 Q8AYL5		Q8AYL5 carassius auratus

085598 PRELIMINARY; PRT; 10 AA.
 Q85598_01-NOV-1996 (TREMBLrel. 01, Created)
 Q85598_01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 Q85598_01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 Moloney murine sarcoma virus (strain HT1) env/mos 5' junction
 (Fragment).
 Moloney murine leukemia virus.
 Viruses; Retroviridae; Gamma-retrovirus.
 NCBI_TaxID=11801;
 RN [1]
 SEQUENCE FROM N.A.
 MEDLINE=83164305; PubMed=6300424;
 RP Donoghue D.J.; Hunter T.;
 RA "Recombination junctions of variants of Moloney murine sarcoma virus: Generation and divergence of a mammalian transforming gene.";
 RT Generation and divergence of a mammalian transforming gene.;
 RL J. Virol. 45:607-617(1983).
 ENB; K03105; AAA46491.; -.
 NON TER 10 10 MW; 1081 MW;
 SEQ 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;
 FPT
 Query Match Score 20; DB 15; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 SVPC 10
 Db 4 STPC 7

RESULT 3
 Q85563 PRELIMINARY; PRT; 10 AA.
 Q85563_01-NOV-1996 (TREMBLrel. 01, Created)
 Q85563_01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 Q85563_01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 Env-mos fusion protein (Fragment).
 Moloney murine leukemia virus.
 Viruses; Retroviridae; Gamma-retrovirus.
 NCBI_TaxID=11801;
 RN [1]
 SEQUENCE FROM N.A.
 MEDLINE=82198891; PubMed=6281735;
 RP Donoghue D.J.; Hunter T.;
 RA "A generalised method of subcloning DNA fragments by restriction site recombination: Application to sequencing the amino-terminal region of the transforming gene of Gazzard murine sarcoma virus.";
 RT Nucleic Acids Res. 10:2549-2564(1982).
 RL [2]
 RN FPT
 Q85563_01-NOV-1996 (TREMBLrel. 01, Created)
 Q85563_01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 Q85563_01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 Env-mos fusion protein (Fragment).
 Moloney murine leukemia virus.
 Viruses; Retroviridae; Gamma-retrovirus.
 NCBI_TaxID=11801;
 RN [1]
 SEQUENCE FROM N.A.
 MEDLINE=82198891; PubMed=6281735;
 RP Donoghue D.J.; Hunter T.;
 RA "A generalised method of subcloning DNA fragments by restriction site recombination: Application to sequencing the amino-terminal region of the transforming gene of Gazzard murine sarcoma virus.";
 RT Nucleic Acids Res. 10:2549-2564(1982).
 RL [2]
 RN FPT
 Q85563_01-NOV-1996 (TREMBLrel. 01, Created)
 Q85563_01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 Q85563_01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 Env-mos fusion protein (Fragment).
 Moloney murine leukemia virus.
 Viruses; Retroviridae; Gamma-retrovirus.
 NCBI_TaxID=11801;

01-NOV-1996 (TREMBLrel. 01, Created)
 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 Moloney murine sarcoma virus (strain HT1) env/mos 5' junction
 (Fragment).
 Moloney murine leukemia virus.
 Viruses; Retroviridae; Gamma-retrovirus.
 NCBI_TaxID=11801;
 RN [1]
 SEQUENCE FROM N.A.
 MEDLINE=83164305; PubMed=6300424;
 RP Donoghue D.J.; Hunter T.;
 RA "Recombination junctions of variants of Moloney murine sarcoma virus: Generation and divergence of a mammalian transforming gene.";
 RT J. Virol. 45:607-617(1983).
 DR EMBL; K03108; AAA46491.; -.
 FT NON TER 10 10 MW; 1081 MW;
 SEQ 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;
 FPT
 Query Match Score 20; DB 15; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 SVPC 10
 Db 4 STPC 7

RESULT 5
 Q56140 PRELIMINARY; PRT; 8 AA.
 Q56140_01-NOV-1996 (TREMBLrel. 01, Created)
 Q56140_01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 Q56140_01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 STP6 Protein (Fragment).
 GN STP6.
 OS Streptococcus thermophilus.
 OB Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=1308;
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN=ST11;
 RC MEDLINE=95047254; PubMed=7958782;
 RA Constable A.; Mollet B.;
 RT "Isolation and characterisation of promoter regions from Streptococcus thermophilus.";
 RL FEMS Microbiol. Lett. 122:85-90(1994).
 DR EMBL; X78210; CA550451.; -.
 FT NON TER 8 8 MW; ED086772D5B045B6 CRC64;
 SEQ 8 AA; 846 MW; ED086772D5B045B6 CRC64;
 FPT
 Query Match Score 19; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ISVP 5
 Db 3 ISVP 6

RESULT 6
 Q7WUG2 PRELIMINARY; PRT; 10 AA.
 Q7WUG2_01-OCT-2003 (TREMBLrel. 25, Created)
 Q7WUG2_01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 Q7WUG2_01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE TrpS1 (Fragment).
 INSA
 GN Escherichia coli.
 OS Plasmid p541.
 OG

RESULT 4
 Q85619 PRELIMINARY; PRT; 10 AA.
 Q85619_01-NOV-1996 (TREMBLrel. 01, Created)
 Q85619_01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 Q85619_01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 Moloney murine sarcoma virus (strain HT1) env/mos 5' junction
 (Fragment).
 Moloney murine leukemia virus.
 Viruses; Retroviridae; Gamma-retrovirus.
 NCBI_TaxID=11801;

OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RN	SEQUENCE FROM N.A.	
OX	Enterobacteriaceae; Escherichia.	RP	RP	
NCBI_TaxID=562;		RESTRAIN=CV_38-11;	and cv.	A632;
[1]		RA	Wilson L.M.; Whitt S.R.; Ibanez A.M.,	Rocheford T.R., Goodman M.M.,
SEQUENCE FROM N.A.		RA		
Caratoli A.; Tzelapi E.;		RA	"Dissection of maize starch production by candidate gene association." ⁱ	
"Antibiotic Resistance Region of an lncN Plasmid Carrying an Integron-Located blaIV-1-Metallo-β-Lactamase Gene and a Novel CMY-Type Cephalosporinase Gene."		RT	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.	
Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.		RL	DR EMBL; AY290305; AAP45331.1; -.	
EMBL: AY339625; AAQ16673.1; -.		DR	DR EMBL; AY290311; AAP45333.1; -.	
KW Plasmid.		FT	NON TER	
FT NON TER	10	9 AA;	976 MW;	DP9BCEA76736C6DD CRC64;
SEQUENCE	10 AA;	991 MW;		
Query Match	33.9%;	Score 19;	DB 20;	Length 9;
Best Local Similarity	57.1%;	Pred. No. 5.8e+03;		
Matches 4;	Conservative	1;	Mismatches 0;	Indels 0;
Db	8 VPC 10			
Db	5 LPC 7			
RESULT 9				
Q96041		PRELIMINARY;		
ID	Q96041	PRT;	10 AA.	
AC	Q96041;			
DT	01-FEB-1997 (TREMBLrel.	02,	Created)	
DT	01-FEB-1997 (TREMBLrel.	02,	Last sequence update)	
DT	01-UN-2003 (TREMBLrel.	24,	Last annotation update)	
DE	NADH ubiquinone oxidoreductase subunit 3 (Fragment).			
GN	NAD3.			
OS	Oenothera berteroana (Bertero's evening primrose).			
OG	Mitochondrion.			
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Onagraceae; Oenothera.			
OX	NCBI_TAXID=3950;			
RN				
SEQUENCE FROM N.A.				
Q9Y4X6		PRELIMINARY;		
ID	Q9Y4X6	PRT;	8 AA.	
AC	Q9Y4X6;			
DT	01-NOV-1995 (TREMBLrel.	12,	Created)	
DT	01-NOV-1999 (TREMBLrel.	12,	Last sequence update)	
DT	01-DIC-2001 (TREMBLrel.	19,	Last annotation update)	
DE	Nuclear LIM interactor (Fragment).			
NL	NLI.			
OS	Homo sapiens (Human).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID=9606;				
[1]				
SEQUENCE FROM N.A.				
RX	MEDLINE=20108806; PubMed=10640831;			
Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S., Schröth A., Bodem J., Royer-Pokora B.;				
"Genomic structure, alternative transcripts and chromosome location of the human LIM domain binding protein gene LDB1.";				
Cytogenet. Cell Genet. 87:119-124 (1999).				
EMBL: AJ243097; CAB45408.1; -.				
FT	NON TER			
SEQ	8 AA;	767 MW;	EE6BDBB862D5B6 CRC64;	
Query Match	30.4%;	Score 17;	DB 4;	Length 8;
Best Local Similarity	60.0%;	Pred. No. 1e+06;		
Matches 3;	Conservative	1;	Mismatches 1;	Indels 0;
Db	6 LSVPC 10			
Db	1 MSVGC 5			
RESULT 10				
Q7X6A3		PRELIMINARY;		
ID	Q7X6A3	PRT;	9 AA.	
AC	Q7X6A3;			
DT	01-OCT-2003 (TREMBLrel.	25,	Created)	
DT	01-OCT-2003 (TREMBLrel.	25,	Last sequence update)	
DT	01-OCT-2003 (TREMBLrel.	25,	Last annotation update)	
DB	Isoamylase (Fragment).			
SUI				
Zea mays subsp. mays (maize).				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
NCBI_TaxID=4578;				

[1] SEQUENCE FROM N.A.

RP STRAIN=Cv. K144;

RC Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M., Buchler E.S. IV;

RA "Dissection of maize starch production by candidate gene association.", RT Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AR290360; AR45386.1; -.

FT NON TER 10 AA; 1063 MW; D0FF9BCA76736C6 CRC64;

SQ SEQUENCE 10 AA; 1063 MW; 34A415B0477B45BB CRC64;

Query Match Score 17; DB 10; Length 10;

Best Local Similarity 66.7%; Pred. No. 1.4e+04;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VPC 10 :||| Db 5 LPC 7

RESULT 11

039557 PRELIMINARY; PRT; 10 AA.

ID 039557; PRELIMINARY; PRT; 10 AA.

AC 039557; (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE E1 protein (Fragment).

OS Hepatitis GB virus C

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC GBV-C/HGV Group.

NCBI TaxID=39539;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Edinburgh haemophiliac;

RA MEDLINE=97368412; PubMed=9225026;

RA Smith D.B., Cuceanu N., Davison P., Jarvis L.M., Mokili J.L., Hamid S., Ludlam C.A., Simmonds P.;

RA "Discrimination of hepatitis G virus/GBV-C geographical variants by RT analysis of the 5' non-coding region.",

RL J. Gen. Virol. 78:1533-1542 (1997).

DR EMBL; AF003175; AAC57986.1; -.

FT NON TER 10 AA; 1067 MW; CC88FB27273772 CRC64;

SQ SEQUENCE 10 AA; 1067 MW; 34A415B0477B45BB CRC64;

Query Match Score 17; DB 12; Length 10;

Best Local Similarity 60.0%; Pred. No. 1.4e+04;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPL 6 :||| Db 1 MAVPL 5

RESULT 12

Q15898 PRELIMINARY; PRT; 8 AA.

ID Q15898; PRELIMINARY; PRT; 8 AA.

AC Q15898; (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE (Clone XP6A11B) (Fragment).

OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI TaxID=9606;

RN SEQUENCE FROM N.A.

RP TISSUE=Placenta.

RC Lee C.-C., Yıldız A., Wehnert M., Bailey J., Couch L., Xiong M., Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y., Caskey C.T.H.;

RT "Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";

RL Hum. Mol. Genet. 0:011995.

DR EMBL; L32078; AAA73888.1; -.

FT NON TER 1 1

FT NON TER 8 8

SQ SEQUENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;

Query Match Score 16; DB 4; Length 8;

Best Local Similarity 60.0%; Pred. No. 1e+06;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SVPLS 7 :||| Db 2 SYPLS 6

RESULT 13

002831 PRELIMINARY; PRT; 8 AA.

ID 002831; PRELIMINARY; PRT; 8 AA.

AC 002831; (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Pro α 1 type III collagen protein (Fragment).

OS Oryctolagus cuniculus (Rabbit).

OC Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.

NCBI TaxID=9886;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=16377339; PubMed=8783186

RA Messaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H., Vuorio E.;

RA "Evidence for insufficient chondrocytic differentiation during repair of full-thickness defects of articular cartilage.";

RA Matrix Biol. 15:39-47(1996).

RL EMBL; S83371; AAD14433.1; -.

KW Collagen.

FT NON TER 1 1

SQ SEQUENCE 8 AA; 1028 MW; B85997272BA77371 CRC64;

Query Match Score 16; DB 6; Length 8;

Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PC 10 :||| Db 3 PC 4

RESULT 14

Q9TRY3 PRELIMINARY; PRT; 8 AA.

ID Q9TRY3; PRELIMINARY; PRT; 8 AA.

AC Q9TRY3; (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE Insulin-like growth factor-binding protein 6, IGFBP-6 (Fragment).

OS Sus scrofa.

OC Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae.

NCBI TaxID=9226;

RN [1]

RP SEQUENCE.

RA MEDLINE=9204376; PubMed=1719383;

RA Shimasaki S., Gao L., Shimonaka M., Ling N.;

RA "Isolation and molecular cloning of insulin-like growth factor-binding protein-6.";

RT Mol. Endocrinol. 5:938-948 (1991).

FT NON TER 1 1

FT NON TER 8 8

SQ SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match Similarity 28.6%; Score 16; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Del 0;

QY	9	PC	10
Db	3	PC	4

RESULT 15

Q8QVD3	Q8QVD3	PRELIMINARY;	PRT;	9 AA.
ID	ID			
AC	Q8QVD3;			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Matrix protein 2 (Fragment).			
GN	M2:			
OS	Ovine respiratory syncytial virus.			
OC	Paramyxoviridae; ssRNA negative-strand viruses; Mononegavirales;			
OC	Parainfluenzavirus; Pneumovirinae; Pneumovirus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21580659; PubMed=11724134;			
RA	Eleraky N.Z., Kania S.A., Potgieter L.N.;			
RT	"The ovine respiratory syncytial virus F gene sequence and its diagnostic application.";			
RT	J. Vet. Diagn. Invest. 13:455-461 (2001).			
RL	EMBL: AF334398; AAC91343.1; -.			
DR	NON-TER 9			
FT	SEQUENCE 9 AA; 1154 MW; 8BGA3EA764541415 CRC64;			
SQ				

Query Match Similarity 28.6%; Score 16; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Del 0;

QY	9	PC	10
Db	6	PC	7

Search completed: September 5, 2004, 11:34:44
 Job time : 58 secs

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Result No.	Score	Query Match Length	DB ID	Description
1	5.6	100.0	10 4 AAU04532	Aau04532 VEGF base
2	41.5	74.1	9 4 AAU04533	Aau04533 VEGF base
3	3.6	64.3	9 2 AAR96138	Aar96138 Protease
4	3.6	64.3	9 2 AAW82212	Aaw82212 D-Norfess-
5	3.6	64.3	9 2 AAM45562	Aam45562 Peptide b
6	3.3	58.9	9 2 AAR96137	Aar96137 Protease
7	3.3	58.9	9 2 AAW82094	Aaw82094 D-Norfess-
8	3.3	58.9	9 2 AAM45561	Aam45561 Peptide b
9	3.3	58.9	9 4 AAG73245	Aag73245 Protease
10	3.3	58.9	9 5 ABU60357	Abu60357 D-Norfess-
11	3.2	57.1	10 4 AAU0643	Aau0643 Human mem
12	3.2	57.1	10 7 ADB88786	Adb88786 Membrane
13	31.5	56.2	9 5 AAU94301	Aau94301 Human nov
14	31.5	56.2	10 5 AAU94201	Aau94201 Human nov
15	31.5	56.2	10 5 AAU94811	Aau94811 Human nov
16	31.5	56.2	10 5 AAU94577	Aau94577 Human nov
17	31	55.4	10 5 AAM5003	Aam5003 Human D40
18	3.0	53.6	9 5 AAU95231	Aau95231 Human nov
19	3.0	53.6	9 5 AAU94696	Aau94696 Human nov
20	3.0	53.6	9 5 AAU95023	Aau95023 Human nov
21	2.9	51.8	10 4 AAG73418	Aag73418 Human gen
22	2.9	51.8	10 4 AAGB5638	Aagb5638 Saccharom
23	2.8	51.8	10 5 ABG4264	Abg4264 Human alb
24	2.8	50.0	9 6 ABR19062	Abr19062 Human can
25	2.8	50.0	10 6 ABR19524	Abr19524 Human can

peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangoma, vascularised malignant or benign tumour, post recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides have also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

Sequence 10 AA;

Query	1 CISVPLSVPCL 10	Score	100.0%	DB	4;	Length	10;
Best Local Similarity	100.0%	Pred. No.	0.0098;				
Matches	10;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps							

Db

1 CISVPLSVPCL 10
1 CISVPLSVPCL 10

PT residues.
XX
PS Claim 49; Page 32; 102pp; English.

CC The sequence represents a monomeric monocyclic peptide of the invention, CC whose 3-dimensional structure is modelled on the expose loop of human VEGF (vascular endothelial growth factor). The invention relates to a CC method of producing a monomeric monocyclic peptide by a measuring beta- CC beta carbon separation distances on opposite antiparallel strands of a CC peptide loop fragment from an exposed loop of a growth factor protein and CC cyclising the peptide by oxidising the cysteine residues. The monocyclic CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic CC peptides), and a cyclic peptide with at least one amino acid deleted prior CC to cyclisation are used to interfere with angiogenesis, CC neovascularisation or lymphangiogenesis in a mammal with a condition CC characterised by angiogenesis, neovascularisation or lymphangiogenesis. CC The condition is diabetic retinopathy, psoriasis, arthropathy, CC hemangoma, vascularised malignant or benign tumour, post-recovery CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold CC trauma, substance-induced neovascularisation of the liver, excessive CC hormone-related angiogenic dysfunction, diabetes induced neovascular CC sequelae, hypertension induced neovascular sequelae, or chronic liver CC infection. The peptides are also used to modulate vascular permeability CC in a mammal (the mammal has a condition characterised by fluid CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, CC or brain). The peptides are used to image blood vessels and lymphatic CC vasculature. The monomeric and bicyclic peptides are used to interfere CC with at least one biological activity induced by VEGF, VEGF-C or -D and CC chronic inflammation, especially rheumatoid arthritis, psoriasis and CC diabetic retinopathy.

SQ Sequence 9 AA;

Query	Match	Score	74.1%	DB	4;	Length	9;
Best Local Similarity	90.0%	Pred. No.	1.4e+06;				
Matches	9;	Conservative	0;	Mismatches	0;	Indels	1;
Gaps							

Oy

1 CISVPLSVPCL 10
1 CISVPL-VPCL 9

RESULT 3

AAR96138

ID AAR96138 standard; peptide; 9 AA.

XX

AC AAR96138;

XX

DT 1 CISTVPL-VPCL 9

Db

Sequence 9 AA;

Query	Match	Score	41.5%	DB	4;	Length	9;
Best Local Similarity	90.0%	Pred. No.	1.4e+06;				
Matches	9;	Conservative	0;	Mismatches	0;	Indels	1;
Gaps							

Oy

1 CISVPLSVPCL 10

1 CISVPL-VPCL 9

Db

Location/Qualifiers

1. 3

/label= C1
/note= "The two conformation determining regions C1 and C2 which flank the protease recognition site Peptide P are provided to position the two fluorophores within 100 angstroms of each other"

1

/note= "labelled by donor fluorophore (F1) 5'- carboxy-tetramethylrhodamine"
4. 7
/label= P
/note= "peptide comprising a protease recognition site"

PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis, PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment, PT from an exposed loop of a growth factor protein by oxidizing the cysteine

PT	Region	8.. ⁹	PD	27-AUG-1998.
FT		/label= C2	XX	
FT		/note- "the two conformation determining regions C1 and	PF	20-FEB-1998;
FT		C2 which flank the protease recognition site peptide P	XX	98WO-US003000.
FT		are provided to position the two fluorophores within 100	PR	20-FEB-1997;
FT		angstroms of each other"	XX	97US-00802981.
FT	Modified-site		PA	(ONCO-) ONCOIMMUNIN INC.
FT			XX	
FT		/note= "labelled by acceptor fluorophore F2 rhodamine X	PI	Komoriya A; Packard BS;
FT		acetamide"	XX	
XX	W09613607-A1.		XX	
PN			DR	WPI; 1998-467579/40.
XX	09-MAY-1996.		XX	
PD			PT	New Fluorogenic compositions - containing 2 fluorophores separated by a
XX	27-OCT-1995;	95WO-US013936.	PT	peptide comprising a protease binding site, used for detecting protease
PR			PT	activity in samples.
XX	28-OCT-1994;	94US-00331383.	XX	
PS			PS	Example 1; Page 52; 90pp; English.
XX	1996-239512/24.		XX	AAWB023-W82240 are peptides used in the construction of a fluorogenic
DR			CC	composition which is used for the detection of protease activity in
XX	PA		CC	biological samples. The products can be used for the detection of
XX	(ONCO-) ONCOIMMUNIN INC.		CC	conformation changes in nucleic acids, oligoaccharides, polysaccharides,
PI			CC	proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins,
XX	Komoriya A; Packard BS;		CC	Steroids or polymers. In addition, attachment of a hydrophobic group to a
XX			CC	molecule can be used to enhance uptake by cells. The composition is
XX			CC	composed of P = peptide comprising a protease binding site for the
DR			CC	protease, F1, F2 peptides = fluorophores where F1 is attached to the
XX	WPI; 1996-239512/24.		CC	amino terminal amino acid and F2 is attached to the carboxyl terminal
XX	PT		CC	amino acid and S1, S2 peptides = when present, are peptide spacers where
PT			CC	S1, when present, is attached to the amino terminal acid, and S2, when
PT			CC	present, is attached to the carboxyl terminal amino acid
XX	Sequence 9 AA:		XX	
SQ			Query Match	Score 36%; DB 2; Length 9;
			Best Local Similarity	50.0%; Pred. No. 1.4e+06;
			Matches 4;	Mismatches 0; Indels 0; Gaps 0;
QY			3 SVPLSVP	10
			: :	2 AIPMSIPC 9
Db			Db	
				RESULT 5
				AAW46562
			ID	AAW46562 standard; peptide; 9 AA.
			XX	
			AC	AAW46562;
			XX	
			DT	20-MAY-1998 (first entry)
			XX	
			DE	Peptide backbone of a protease indicator.
			XX	
			KW	Protease binding site; protease; protease indicator; fluorescent signal;
			KW	detection; protease activity.
			XX	
			OS	Synthetic.
			XX	
			PN	US5714342-A.
			XX	
			PD	03-FEB-1998.
			XX	
			PF	27-OCT-1995;
			XX	95US-00549008.
			PR	28-OCT-1994;
			XX	94US-00331383.
			PA	(ONCO-) ONCOIMMUNIN INC.
			XX	
			PI	Packard BS, Komoriya A;
			XX	
			DR	WPI; 1998-158345/14.
			XX	
			PT	Fluorogenic substrates for protease determination - having two closely
			OS	
			XX	
			PN	
			XX	

PT spaced fluorophores flanking protease binding site.
 XX Example 1; Col 23; 39pp; English.
 CC The present peptide contains a protease binding site. It is used to
 CC produce novel reagents whose fluorescence increases in the presence of
 CC particular proteases. These fluorogenic protease indicators (substrates)
 CC provide a high intensity fluorescent signal at a visible wavelength when
 CC they are digested by a protease. The fluorogenic indicators have the
 CC general formula: F1--Cl--P2 | (S1)n (S2)k where: P is a peptide
 CC containing a protease binding site e.g. AAW46520-53. F1 and F2
 CC are fluorophores. S1 and S2 are peptide spacers e.g. AAW45554-58. n, k =
 CC 0 or 1. Cl and C2 are conformation-determining regions that introduce a
 CC bend into the composition which positions the fluorophores adjacent to
 CC each other with a separation of less than 100 Angstrom. When n is 1, S1
 CC is joined to the terminal alpha -amino group of C1 by a peptide bond, and
 CC when k is 1, S2 is joined to the terminal carboxy group of C2 by a
 CC peptide bond. The protease indicators are used for detecting protease
 CC activity in a biological sample. The sample is contacted with the
 CC indicator and any change in fluorescence is detected, an increase in
 CC fluorescence indicating protease activity
 XX Sequence 9 AA;
 SQ Query Match 64.3%; Score 36; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVPLSVPC 10
 ::|:|:
 2 AIPMSIPC 9
 DB

RESULT 6
 AAR96137 standard; peptide; 9 AA.
 XX
 AC AAR96137;
 XX DT 25-MAR-2003 (revised)
 DT 18-DEC-1996 (first entry)
 XX DE Protease substrate peptide with fluorophore at each terminus.
 DE KW Fluorogenic substrate; fluorophore; protease activity; assay;
 KW visible fluorescence; in situ detection; frozen tissue section;
 KW histology; arthritis; thrombosis; emphysema; cancer metastasis.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 FR Region 1..3
 FR /label= C1
 FT /note= "the two conformation determining regions C1 and
 FT C2 which flank the protease recognition site peptide P
 FT are provided to position the two fluorophores within 100
 FT angstroms of each other."
 FT Modified-site 1
 FT /note= "labelled by donor fluorophore (F1) 5'-
 FT carboxy-tetramethylrhodamine"
 FT Peptide 4..7
 FT /label= P
 FT /note= "peptide comprising a protease recognition site"
 FT Modified-site 5
 FT /label= Nle
 FT 8..9
 FT /label= C2
 FT /note= "the two conformation determining regions C1 and
 FT C2 which flank the protease recognition site peptide P
 FT are provided to position the two fluorophores within 100
 FT angstroms of each other."
 FT Modified-site 9
 FT /note= "labelled by acceptor fluorophore F2 rhodamine X

FT acetamide"
 XX WO9613607-A1.
 PN XX 09-MAY-1996.
 PD XX 27-OCT-1995; 95WO-US013936.
 PF XX 28-OCT-1994; 94US-0331383.
 PR XX (ONCO-) ONCOIMMUNIN INC.
 PA XX PI Konoriya A, Packard BS;
 DR WPI; 1996-239512/24.
 PT New fluorogenic peptide(s) with fluorophore at each terminus - for
 PT detecting protease(s) in biological samples, emit intense visible
 PT fluorescence when cleaved.
 XX PS Claim 15; Page 31; 88PP; English.
 XX The present sequence is a specific example of a fluorogenic substrate for
 CC detecting activity of a protease. The substrate agrees with the generic
 CC formula (S1)n-C1(F1)-Pc2(F2)k in which a peptide P of 2-8 amino
 CC acids comprising a recognition site for the protease is flanked by
 CC conformation determining regions (C1 and C2) of 1-3 amino acids. C1 and
 CC C2 are labelled by fluorophore groups (F1 and F2, respectively)
 CC positioned within 100 angstroms of each other. Additional peptide spacers
 CC of 1-50 amino acids (S1 and S2) may also be present (i.e. n and k = 0 or
 CC 1). Fluorogenic substrates corresponding to the generic formula are used
 CC to detect or localise proteases in biological specimens, esp. in frozen
 CC tissue sections or to monitor protease activity in stored reagents.
 CC Changes in protease activity are associated with e.g. arthritis,
 CC emphysema, thrombosis and cancer metastasis. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX SQ Sequence 9 AA;
 Query Match 58.9%; Score 33; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SVPLSVPC 10
 ::|:|:
 Db 2 AIPMSIPC 9
 RESULT 7
 ID AAN82094
 ID AAN82094 standard; peptide; 9 AA.
 XX AC AAN82094;
 XX AC
 XX DT 18-FEB-1999 (first entry)
 XX DE D-Norfes-A protease inhibitor peptide.
 XX KW Protease activity; fluorophore; detection; fluorogenic; cellular uptake;
 KW conformation change.
 XX OS Synthetic.
 XX FH Location/Qualifiers
 FR Key
 FR Region
 FR /label= C1
 FT /note= "Asp residue is modified by the presence of F1
 where F1 is the donor fluorophore 5'-
 carboxytetramethylrhodamine (C2211)"
 FT Modified-site 1
 FT /label= Nle
 FT 8..9
 FT /label= C2
 FT /note= "the two conformation determining regions C1 and
 FT C2 which flank the protease recognition site peptide P
 FT are provided to position the two fluorophores within 100
 FT angstroms of each other."
 FT Modified-site 5
 FT /note= "Norleucine"
 FT 9
 FT /note= "Cys residue is modified by the presence of F2
 FT

where F2 is the acceptor fluorophore rhodamine X acetamide (R492);

XX PR 28-OCT-1994; 94US-00333383.

FT XX

XX PA

XX (ONCO-) ONCOMMUNIN INC.

XX PI

XX Packard BS,

XX Komoriya A;

XX DR WPI; 1998-158345/14.

PT Fluorogenic substrates for protease determination - having two closely spaced fluorophores flanking protease binding site.

PA Example 1; Col 23; 39pp; English.

XX PS

XX

The present peptide contains a protease binding site. It is used to produce novel reagents whose fluorescence increases in the presence of particular proteases. These fluorogenic protease indicators (substrates) provide a high intensity fluorescent signal at a visible wavelength when they are digested by protease. The fluorogenic indicators have the general formula: F1--C1--P--C2--F2 | (S1) (S2)k where: P is a peptide containing a protease binding site e.g. AAW45520-53, AAW46560. F1 and F2 are fluorophores. S1 and S2 are peptide spacers e.g. AAW45554-58 n, k = 0 or 1. C1 and C2 are conformation determining regions that introduce a bend into the composition which positions the fluorophores adjacent to each other with the separation of less than 100 Angstrom. When n is 1, S1 is joined to the terminal alpha -amino group of C1 by a peptide bond, and when k is 1, S2 is joined to the terminal carboxyl group of C2 by a peptide bond. The protease indicators are used for detecting protease activity in a biological sample. The sample is contacted with the indicator and any change in fluorescence is detected, an increase in fluorescence indicating protease activity

XX Sequence 9 AA:

XX

XX</p

PR	10-SEP-1999;	99US-00394019.		
XX	(ONCO-) ONCOMMUNIN INC.			
PA				
XX	Komoriya A,	Packard BS;		
PI				
XX	WPI; 2001-389573/41.			
XX	New fluorogenic compositions whose fluorescence level increases in the presence of active proteases, useful for detecting and localizing protease activity in biological samples, particularly in frozen tissue samples.			
PS	Example 2; Page 53; 86pp; English.			
XX	The present invention describes fluorogenic compositions which can be used for the detection of protease activity. This can be useful as an indicator of viral infection, cancer metastasis, haemophilia, emphysema, thrombosis and arthritis. The fluorogenic compositions comprise a peptide, a peptide spacer and a donor and an acceptor fluorophore. The peptide is cleaved by a protease and the fluorophores can then be detected. The present sequence is one of the peptides described in the exemplification of the invention			
SQ	Sequence 9 AA;			
	Query Match	58.9%; Score 33; DB 4; Length 9;		
	Best Local Similarity	50.0%; Pred. No. 1.4e+06;		
	Matches	4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;		
QY	3 SVPLSVPC 10			
DB	:: : : : 2 AIKPSIPC 9			
	RESULT 10			
	ABU60357			
ID	ABU60357 standard; peptide; 9 AA.			
XX	ABU60357;			
AC				
XX	DT 29-APR-2003 (first entry)			
XX	DB D-NorFES-A protease inhibitor peptide.			
XX	Protease; indicator; chromophore; H-dimer; fluorescence; absorbance; KW nuclease; screening; fluorophore; substrate cleavage.			
OS	Synthetic.			
FH	Location/Qualifiers			
FT	Modified-site 1 /note= "F1, where F1 is a donor fluorophore 5'-			
FT	carboxytertbutylrhodamine (C211)"			
FT	Modified-site 5 /label= "Nle			
FT	/note= "norleucine"			
FT	Modified-site 9 /note= "F2, where F2 is an acceptor fluorophore rhodamine X acetamide (R492)"			
FT				
XX	WO200261038-A2.			
XX	08-AUG-2002.			
XX	21-DEC-2001; 2001WO-US049781.			
PR	22-DEC-2000; 2000US-00747287.			
XX	(ONCO-) ONCOMMUNIN INC.			
PA	Packard BS, Komoriya A;			
XX				
PI	Homo sapiens			
XX				
DR	WPI; 2002-698548/75.			
XX	Indicator composition comprising polypeptide or nucleic acid backbone PT joining two same chromophores resulting in quenching of fluorescence PT of change in absorbance of chromophores, useful for detecting protease PT activity.			
XX	Example 2; Page 15; 97pp; English.			
XX	This invention describes a novel indicator composition (referred as homodoubly labeled composition) comprising a polypeptide backbone or a nucleic acid backbone joining two chromophores of the same species whereby the chromophores form an H-dimer resulting in quenching of the fluorescence of or a change in absorbance of the chromophore, a decrease in fluorescence or a change in absorbance indicates that the first molecule and the second molecule are interacting. The indicator is useful for detecting the activity of a protease, where an increase in fluorescence or a change in absorbance indicates that the protease cleaves the polypeptide backbone. The indicator is attached to a solid support inside a mammalian, yeast or insect cell. The composition bears a hydrophobic group such as EMOC, 9-fluorene carboxylic group, and 9-fluorenone-1-carboxylic group, benzyloxycarbonyl (Xan), Trityl (Trt), 4-methoxy-2,3,6-trimethylbenzenesulphonyl (Mts), Mesitylene-2-sulphonyl (Mts), 4,4'-(dimethoxybenzhydryl (Mbs), etc. The method described in the invention is useful for detecting protease or nuclease activity (or the presence of nucleic acid) in histological section, cells in culture, (e.g., seeded or cultured adherent cells), a biological sample such as tissue, biopsy, lymph, embryo, or whole animal, or cell suspension derived from a biological sample such as tissue, blood, urine, aliv, lymph, or biopsy. The indicator composition is also useful for screening a test agent for the ability to modulate a protease (or a nuclease, lipase, etc.). The indicator reagents allow rapid determination of protease activity in a matter of minutes in a single-step procedure. The fluorescent indicators both absorb and emit in the visible range (400-800 nm). These signals are therefore not readily quenched by, nor is activation of the fluorophores; that is, absorption of light, interfered with by background molecules; therefore they are easily detected in biological samples. The fluorogenic protease indicators utilise high efficiency fluorophores and are able to achieve a high degree of quenching while providing a strong signal when the quench is released by cleavage of the peptide substrate. The high signal allows detection of very low levels of protease activity. Thus the fluorogenic protease indicators are particularly well suited for <i>in situ</i> detection of protease activity. ABU60357-ABU60477 represent peptides used to illustrate the method described in the disclosure of the invention			
SQ	Sequence 9 AA;			
	Query Match	58.9%; Score 33; DB 5; Length 9;		
	Best Local Similarity	50.0%; Pred. No. 1.4e+06;		
	Matches	4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;		
QY	3 SVPLSVPC 10			
DB	:: : : 2 AIKPSIPC 9			
	RESULT 11			
	AAU00643			
ID	AAU00643 standard; peptide; 10 AA.			
XX	AAU00643;			
AC				
XX	DT 07-SEP-2001 (first entry)			
XX	DE Human membrane translocating peptide (MTLP) #12.			
XX	KW Membrane translocating peptide; MTLP; human; intracellular gene delivery;			
XX	KW epithelial cell layer; gastrointestinal tract; circulatory system.			
OS				

DR WPI; 2002-269179/31.
 XX PD 21-FEB-2002.
 PT Monitoring 83P2H3 gene products for monitoring the presence of cancer in
 a subject, comprising determining the status of 83P2H3 gene products in a
 tissue sample from the subject and comparing it to a normal sample.
 XX PR 17-AUG-2001; 2001WO-US025782.
 PT 17-AUG-2000; 2000US-0226329P.
 XX PA (AGENSYN) AGENSYS INC.
 CC Raitano AB, Challita-Bid PM, Paris M, Saffran DC, Afar DEH;
 CC Levin E, Hubert RS, Ge W, Jakobovits A;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 XX WPI; 2002-266179/31.
 PT Monitoring 83P2H3 gene products for monitoring the presence of cancer in a
 subject, comprises determining the status of 83P2H3 gene products in a
 tissue sample from the subject and comparing it to a normal sample.
 XX (AgenSyn) AGENSYS INC.
 CC The invention relates to monitoring 83P2H3 (a calcium transport protein
 whose gene is located on chromosome 7q34) gene products in a biological
 sample from a patient who has or is suspected of having cancer
 (especially prostate cancer), comprises: (a) determining the status of
 83P2H3 gene products expressed by cells in a tissue sample from an
 individual and (b) comparing the status to the status of 83P2H3 gene
 products in a normal sample. Also included are modulators of 83P2H3
 function or status, generating antibodies/immune response against 83P2H3
 (or related protein CatTF2E11 (human leukocyte antigen) binding peptides
 12Q24.1) using identified HLA (human leukocyte antigen) gene located on chromosome
 12Q24.1) using identified HLA (human leukocyte antigen) binding peptides
 derived from the protein, delivering a cytotoxic agent to a cell
 expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
 recombinant protein comprising an antigen-binding region of the antibody,
 a non-human transgenic animal that produces the recombinant protein, a
 hybridoma that produces the recombinant protein, a single-chain
 monoclonal antibody that comprises the variable domains of the heavy and
 light chains of the anti-83P2H3 antibody, a vector comprising a
 polynucleotide that encodes the monoclonal antibody and inducing an
 immune response to a 83P2H3 protein, by providing a 83P2H3-related
 protein that comprises a T cell or B cell epitope, and contacting the
 epitope with an immune system T cell or B cell, respectively. The method
 is useful for monitoring 83P2H3 gene products in a biological sample for
 monitoring the presence of cancer in an individual. The modulator is
 useful for inhibiting the growth of cancer cells that express 83P2H3, for
 treating cancer and the vector is useful for treating a patient with a
 cancer that expresses 83P2H3. The immunological methods are useful for
 generating an immune response against 83P2H3, and for detecting the
 presence of 83P2H3-related protein or polynucleotide in a biological
 sample from a patient who has or who is suspected of having cancer. The
 antibody is useful in prostate cancer diagnosis, prognosis, imaging
 methodologies and treatment, to detect and quantify 83P2H3 and mutant
 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 isolating 83P2H3 homologues/related molecules, and for generating anti-
 idotypic antibodies that mimic the 83P2H3 protein. The present sequence
 is an HLA binding peptide motif from 83P2H3 or its related protein
 CatTF2E11
 XX Sequence 9 AA;
 SQ Query Match 56.2%; Score 31.5; DB 5; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 2; Nismatches 1; Indels 1; Gaps 1;
 YY 1 C1SVP1SLVPC 10
 DE Human novel protein CatTF2E11 HLA binding peptide #84.
 AC AAU94201;
 DT 02-JUL-2002 (First entry)
 XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CatTF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW Chromosome 7q4;
 XX WO200214361-A2.
 OS Homo sapiens.
 PN AAU94811 standard; peptide; 10 AA.
 XX AAU94811;
 AC AAU94811;
 XX AAU94811;
 PT RESULT 15
 ID AAU94811
 DB 1 CLT-PLSFP/C 9
 QY 1 C1SVP1SLVPC 10
 DE Human novel protein CatTF2E11 HLA binding peptide #84.
 AC AAU94201;
 DT 02-JUL-2002 (First entry)
 XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CatTF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW Chromosome 7q4;
 XX WO200214361-A2.
 OS Homo sapiens.
 PN AAU94811;

XX 02-JUL-2002 (first entry)
 DT XX Human novel protein CatRP2E11 HLA binding peptide #394.
 DE XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CatRP2E11;
 KW XX calcium transport protein; cancer; prostate cancer; cytostatic;
 KW XX chromosome 7q34; chromosome 12q24.1; T cell; B cell.
 OS XX Homo sapiens.
 XX WO200214361-A2.
 XX PD 21-FEB-2002.
 XX PF 17-AUG-2001; 2001WO-US025782.
 XX PR 17-AUG-2000; 2000US-0226329P.
 XX PA (AGEN-) AGENSYN INC.
 XX PI Raitano AB, Challita-Bid PM, Faris M, Saffran DC, Afar DEH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 XX DR 2002-269179/31.
 XX PT Monitoring 83P2H3 gene products for monitoring the presence of cancer in
 PT a subject comprises determining the status of 83P2H3 gene products in a
 PT tissue sample from the subject and comparing it to a normal sample.
 XX Example 11; Page 191; 270pp; English.
 XX The invention relates to monitoring 83P2H3 (a calcium transport protein
 CC whose gene is located on chromosome 7q34) gene products in a biological
 CC sample from a patient who has or is suspected of having cancer
 CC (especially prostate cancer), comprises: (a) determining the status of
 CC 83P2H3 gene products expressed by cells in a tissue sample from an
 CC individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against 83P2H3
 CC (or related protein) CatRP2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
 CC derived from the protein, delivering a cytotoxic agent to a cell
 CC expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
 CC recombinant protein comprising an antigen-binding region of the antibody,
 CC a non-human transgenic animal that produces the recombinant protein, a
 CC hybridoma that produces the recombinant protein, a single-chain
 CC monoclonal antibody that comprises the variable domains of the heavy and
 CC light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively; The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules and for generating anti-
 CC idotypic antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CatRP2E11

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OM protein - protein search, using SW mode.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	9 US-09-761-636A-13	Sequence 13, Appl
2	41.5	74.1	9	9 US-09-761-636A-14	Sequence 14, Appl
3	33	58.9	9	12 US-09-74-207-A	Sequence 1, Appl
4	33	58.9	9	12 US-09-874-350A-1	Sequence 1, Appl
5	33	58.9	9	12 US-09-874-350A-184	Sequence 184, Appl
6	32	57.1	10	14 US-10-126-845-13	Sequence 13, Appl
7	32	57.1	10	14 US-10-126-845-71	Sequence 71, Appl
8	32	57.1	10	15 US-10-116-215-101	Sequence 101, Appl
9	32	57.1	10	16 US-10-764-335-13	Sequence 13, Appl
10	31	56.2	9	10 US-09-932-165-284	Sequence 284, Appl
11	31.5	56.2	10	10 US-09-932-165-184	Sequence 184, Appl
12	31.5	56.2	10	10 US-09-932-165-560	Sequence 560, Appl
13	31.5	56.2	10	10 US-09-932-165-794	Sequence 794, Appl
14	31	55.4	9	15 US-10-154-884B-11221	Sequence 11221, A
15	31	55.4	10	12 US-10-363-791-194	Sequence 194, App

RESULTS

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0%	10	9 US-09-761-636A-13	Organism: Homo sapiens
Qy		Query Match	100.0%	Score 56; DB 9;	Length 10;
Db		Best Local Similarity	100.0%; Pred. No. 0.023;	Mismatches 0;	Indels 0;
		Matches 10;	Conservative	0;	Gaps 0;

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	9 US-09-761-636A-13	Sequence 13, Appl
2	41.5	74.1	9	9 US-09-761-636A-14	Sequence 14, Appl
3	33	58.9	9	12 US-09-74-207-A	Sequence 1, Appl
4	33	58.9	9	12 US-09-874-350A-1	Sequence 1, Appl
5	33	58.9	9	12 US-09-874-350A-184	Sequence 184, Appl
6	32	57.1	10	14 US-10-126-845-13	Sequence 13, Appl
7	32	57.1	10	14 US-10-126-845-71	Sequence 71, Appl
8	32	57.1	10	15 US-10-116-215-101	Sequence 101, Appl
9	32	57.1	10	16 US-10-764-335-13	Sequence 13, Appl
10	31	56.2	9	10 US-09-932-165-284	Sequence 284, Appl
11	31.5	56.2	10	10 US-09-932-165-184	Sequence 184, Appl
12	31.5	56.2	10	10 US-09-932-165-560	Sequence 560, Appl
13	31.5	56.2	10	10 US-09-932-165-794	Sequence 794, Appl
14	31	55.4	9	15 US-10-154-884B-11221	Sequence 11221, A
15	31	55.4	10	12 US-10-363-791-194	Sequence 194, App

RESULTS

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0%	10	9 US-09-761-636A-13	Sequence 13, Appl
Qy		Query Match	100.0%	Score 56; DB 9;	Length 10;
Db		Best Local Similarity	100.0%; Pred. No. 0.023;	Mismatches 0;	Indels 0;
		Matches 10;	Conservative	0;	Gaps 0;

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	9 US-09-761-636A-13	Sequence 13, Appl
2	41.5	74.1	9	9 US-09-761-636A-14	Sequence 14, Appl
3	33	58.9	9	12 US-09-74-207-A	Sequence 1, Appl
4	33	58.9	9	12 US-09-874-350A-1	Sequence 1, Appl
5	33	58.9	9	12 US-09-874-350A-184	Sequence 184, Appl
6	32	57.1	10	14 US-10-126-845-13	Sequence 13, Appl
7	32	57.1	10	14 US-10-126-845-71	Sequence 71, Appl
8	32	57.1	10	15 US-10-116-215-101	Sequence 101, Appl
9	32	57.1	10	16 US-10-764-335-13	Sequence 13, Appl
10	31	56.2	9	10 US-09-932-165-284	Sequence 284, Appl
11	31.5	56.2	10	10 US-09-932-165-184	Sequence 184, Appl
12	31.5	56.2	10	10 US-09-932-165-560	Sequence 560, Appl
13	31.5	56.2	10	10 US-09-932-165-794	Sequence 794, Appl
14	31	55.4	9	15 US-10-154-884B-11221	Sequence 11221, A
15	31	55.4	10	12 US-10-363-791-194	Sequence 194, App

RESULTS

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0%	10	9 US-09-761-636A-13	Sequence 13, Appl
Qy		Query Match	100.0%	Score 56; DB 9;	Length 10;
Db		Best Local Similarity	100.0%; Pred. No. 0.023;	Mismatches 0;	Indels 0;
		Matches 10;	Conservative	0;	Gaps 0;

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	9 US-09-761-636A-13	Sequence 13, Appl
2	41.5	74.1	9	9 US-09-761-636A-14	Sequence 14, Appl
3	33	58.9	9	12 US-09-74-207-A	Sequence 1, Appl
4	33	58.9	9	12 US-09-874-350A-1	Sequence 1, Appl
5	33	58.9	9	12 US-09-874-350A-184	Sequence 184, Appl
6	32	57.1	10	14 US-10-126-845-13	Sequence 13, Appl
7	32	57.1	10	14 US-10-126-845-71	Sequence 71, Appl
8	32	57.1	10	15 US-10-116-215-101	Sequence 101, Appl
9	32	57.1	10	16 US-10-764-335-13	Sequence 13, Appl
10	31	56.2	9	10 US-09-932-165-284	Sequence 284, Appl
11	31.5	56.2	10	10 US-09-932-165-184	Sequence 184, Appl
12	31.5	56.2	10	10 US-09-932-165-560	Sequence 560, Appl
13	31.5	56.2	10	10 US-09-932-165-794	Sequence 794, Appl
14	31	55.4	9	15 US-10-154-884B-11221	Sequence 11221, A
15	31	55.4	10	12 US-10-363-791-194	Sequence 194, App

RESULTS

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0%	10	9 US-09-761-636A-13	Sequence 13, Appl
Qy		Query Match	100.0%	Score 56; DB 9;	Length 10;
Db		Best Local Similarity	100.0%; Pred. No. 0.023;	Mismatches 0;	Indels 0;
		Matches 10;	Conservative	0;	Gaps 0;

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	9 US-09-761-636A-13	Sequence 13, Appl
2	41.5	74.1	9	9 US-09-761-636A-14	Sequence 14, Appl
3	33	58.9	9	12 US-09-74-207-A	Sequence 1, Appl
4	33	58.9	9	12 US-09-874-350A-1	Sequence 1, Appl
5	33	58.9	9	12 US-09-874-350A-184	Sequence 184, Appl
6	32	57.1	10	14 US-10-126-845-13	Sequence 13, Appl
7	32	57.1	10	14 US-10-126-845-71	Sequence 71, Appl
8	32	57.1	10	15 US-10-116-215-101	Sequence 101, Appl
9	32	57.1	10	16 US-10-764-335-13	Sequence 13, Appl
10	31	56.2	9	10 US-09-932-165-284	Sequence 284, Appl
11	31.5	56.2	10	10 US-09-932-165-184	Sequence 184, Appl
12	31.5	56.2	10	10 US-09-932-165-560	Sequence 560, Appl
13	31.5	56.2	10	10 US-09-932-165-794	Sequence 794, Appl
14	31	55.4	9	15 US-10-154-884B-11221	Sequence 11221, A
15	31	55.4	10	12 US-10-363-791-194	Sequence 194, App

RESULTS

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0%	10	9 US-09-761-636A-13	Sequence 13, Appl
Qy		Query Match	100.0%	Score 56; DB 9;	Length 10;
Db		Best Local Similarity	100.0%; Pred. No. 0.023;	Mismatches 0;	Indels 0;
		Matches 10;	Conservative	0;	Gaps 0;

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	9 US-09-761-636A-13	Sequence 13, Appl
2	41.5	74.1	9	9 US-09-761-636A-14	Sequence 14, Appl
3	33	58.9	9	12 US-09-74-207-A	Sequence 1, Appl
4	33	58.9	9	12 US-09-874-350A-1	Sequence 1, Appl
5	33	58.9	9	12 US-09-874-350A-184	Sequence 184, Appl
6	32	57.1	10	14 US-10-126-845-13	Sequence 13, Appl
7	32	57.1	10	14 US-10-126-845-71	Sequence 71, Appl
8	32	57.1	10	15 US-10-116-215-101	Sequence 101, Appl
9	32	57.1	10	16 US-10-764-335-13	Sequence 13, Appl
10	31	56.2	9	10 US-09-932-165-284	Sequence 284, Appl
11	31.5	56.2	10	10 US-09-932-165-184	Sequence 184, Appl
12	31.5	56.2	10	10 US-09-932-165-560	Sequence 560, Appl
13	31.5	56.2	10	10 US-09-932-165-794	Sequence 794, Appl
14	31	55.4	9	15 US-10-154-884B-11221	Sequence 11221, A
15	31	55.4	10	12 US-10-363-791-194	Sequence 194, App

RESULTS

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0%	10	9 US-09-761-636A-13	Sequence 13, Appl
Qy		Query Match	100.0%	Score 56; DB 9;	Length 10;
Db		Best Local Similarity	100.0%; Pred. No. 0.023;	Mismatches 0;	Indels 0;
		Matches 10;	Conservative	0;	Gaps 0;

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	9 US-09-761-636A-13	Sequence 13, Appl
2	41.5	74.1	9	9 US-09-761-636A-14	Sequence 14, Appl
3	33	58.9	9	12 US-09-74-207-A	Sequence 1, Appl
4	33	58.9	9	12 US-09-874-350A-1	Sequence 1, Appl
5	33	58.9	9	12 US-09-874-350A-184	Sequence 184, Appl
6	32	57.1	10	14 US-10-126-845-13	Sequence 13, Appl
7	32	57.1	10	14 US-10-126-845-71	Sequence 71, Appl
8	32	57.1	10	15 US-10-116-215-101	Sequence 101, Appl
9	32	57.1	10	16 US-10-764-335-13	Sequence 13, Appl
10	31	56.2	9	10 US-09-932-165-284	Sequence 284, Appl
11	31.5	56.2	10	10 US-09-932-165-184	Sequence 184, Appl
12	31.5	56.2	10	10 US-09-932-165-560	Sequence 560, Appl
13	31.5	56.2	10	10 US-09-932-165-794	Sequence 794, Appl
14	31	55.4	9	15 US-10-154-884B-11221	Sequence 11221, A
15	31	55.4	10	12 US-10-363-791-194	Sequence 194, App

RESULTS

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0%	10	9 US-09-761-636A-13	Sequence 13, Appl
Qy		Query Match	100.0%	Score 56; DB 9;	Length 10;
Db		Best Local Similarity	100.0%; Pred. No. 0.023;	Mismatches 0;	Indels 0;
		Matches 10;	Conservative	0;	Gaps 0;

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	9 US-09-761-636A-13	Sequence 13, Appl
2	41.5	74.1	9	9 US-09-761-636A-14	Sequence 14, Appl
3	33	58.9	9	12 US-09-74-207-A	Sequence 1, Appl
4	33	58.9	9	12 US-09-874-350A-1	Sequence 1, Appl
5	33	58.9	9	12 US-09-874-350A-184	Sequence 184, Appl
6	32	57.1	10	14 US-10-126-845-13	Sequence 13, Appl
7	32	57.1	10	14 US-10-126-845-71	Sequence 71, Appl
8	32	57.1	10	15 US-10-116-215-101	Sequence 101

GENERAL INFORMATION:
 APPLICANT: ACHEN, Marc
 APPLICANT: STACKER, Steven
 APPLICANT: HUGHES, Richard
 APPLICANT: CENDRON, Angela
 TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
 FILE REFERENCE: 1054/48505 Achen et al
 CURRENT APPLICATION NUMBER: US/09/761,636A
 CURRENT FILING DATE: 2001-01-18
 PRIOR APPLICATION NUMBER: US 60/175,293
 PRIOR FILING DATE: 2000-01-18
 PRIOR APPLICATION NUMBER: US/09/204,590
 PRIOR FILING DATE: 2000-05-16
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 14
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-761-636A-14

Query Match 74.1% Score 41.5%; DB 9; Length 9;
 Best Local Similarity 90.0%; Pred. No. 1.2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVPLSVPC 10
 Db 1 CISVPL-VPC 9

RESULT 3
 US-09-747-287-1

Sequence 1, Application US/09747287
 Publication No. US20030207264A1

GENERAL INFORMATION:
 APPLICANT: KOMORIYA, AKIRA
 APPLICANT: PACKARD, BEVERLY S.
 TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL SAMPLES
 FILE REFERENCE: 300-9486001S
 CURRENT APPLICATION NUMBER: US/09/747,287
 PRIOR APPLICATION NUMBER: US 60/12-22
 PRIOR FILING DATE: 1999-09-10
 PRIOR APPLICATION NUMBER: US/08/802,981
 PRIOR FILING DATE: 1997-02-20
 PRIOR FILING DATE: 2000-09-11
 NUMBER OF SEQ ID NOS: 242
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 1
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Synthetic peptide.

NAME/KEY: misc_feature
 LOCATION: (5)..(5)
 OTHER INFORMATION: Xaa is norleucine

US-09-747-287-1

Query Match 58.9% Score 33; DB 12; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.2e+06;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SVPLSVPC 10
 Db 2 AIPXSPC 9

RESULT 4
 US-09-874-350A-1

US-09-874-350A-184

Query Match 58.9%; Score 33; DB 12; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.2e+06;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 CISVPLSVPC 10
 Db 2 AIPKSIPC 9

RESULT 6
 US-10-126-845-13
 ; Sequence 13, Application US/10126845
 ; Publication No. US20030181367A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Mahony, Daniel J.
 ; APPLICANT: Lambkin, Imelda J.
 ; APPLICANT: Pinilla, Clemencia
 ; APPLICANT: Houghton, Richard
 ; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
 ; FILE REFERENCE: E1067/20058
 ; CURRENT APPLICATION NUMBER: US/10/126,845
 ; CURRENT FILING DATE: 2002-10-15
 ; NUMBER OF SEQ ID NOS: 119
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: membrane translocating peptide, cyclic
 US-10-126-845-13

Query Match 57.1%; Score 32; DB 14; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 CISVPLSVPC 10
 Db 1 CLPVLLAAPC 10

RESULT 7

US-10-126-845-71
 ; Sequence 71, Application US/10126845
 ; Publication No. US20030181367A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Mahony, Daniel J.
 ; APPLICANT: Lambkin, Imelda J.
 ; APPLICANT: Pinilla, Clemencia
 ; APPLICANT: Houghton, Richard
 ; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
 ; FILE REFERENCE: E1067/20058
 ; CURRENT APPLICATION NUMBER: US/10/126,845
 ; CURRENT FILING DATE: 2002-10-15
 ; NUMBER OF SEQ ID NOS: 119
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 71
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: D form peptide

NAME/KEY: MISC FEATURE
 LOCATION: (1)-(10)
 OTHER INFORMATION: D form amino acid
 US-10-126-845-71

Query Match 57.1%; Score 32; DB 14; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CISVPLSVPC 10
 Db 1 CLPVLLAAPC 10

RESULT 8
 US-10-116-275-101
 ; Sequence 101, Application US/10116275
 ; Publication No. US20030211476A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Elan Pharmaceutical Technology
 ; APPLICANT: O'Mahony, Daniel J.
 ; APPLICANT: Brayden, David
 ; APPLICANT: Byrne, Daragh
 ; APPLICANT: Lambkin, Imelda
 ; APPLICANT: Higgins, Lisa

; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
 ; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
 ; FILE REFERENCE: E1167/20087
 ; CURRENT APPLICATION NUMBER: US/10/116,275
 ; CURRENT FILING DATE: 2002-10-04
 ; NUMBER OF SEQ ID NOS: 349
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 101
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance Uc
 ; OTHER INFORMATION: take Across the GIT"
 US-10-116-275-101

Query Match 57.1%; Score 32; DB 15; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 CISVPLSVPC 10
 Db 1 CLPVLLAAPC 10

RESULT 9

US-10-764-235-13
 ; Sequence 13, Application US/10764235
 ; Publication No. US20040138132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Mahony, Daniel J.
 ; APPLICANT: Lambkin, Imelda J.
 ; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
 ; FILE REFERENCE: P226-479-B-USA
 ; CURRENT APPLICATION NUMBER: US/10/764,235
 ; CURRENT FILING DATE: 2004-01-23
 ; PRIOR APPLICATION NUMBER: 09/671,089
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/156,246
 ; PRIOR FILING DATE: 1999-09-27
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: membrane translocating peptide, cyclic

US-10-764-235-13

Query Match 57.1%; Score 32; DB 16; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 CISVPLSVPC 10
 ; : | : |

Db 1 CLPVLLAAPC 10

RESULT 10

US-09-932-165-284

; Sequence 284, Application US/09932165

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: PARIS, MARY

; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBIVITS, AYA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND

; TITLE OF INVENTION: DETECTION OF CANCER

; FILE REFERENCE: 51158-20014.00

; CURRENT APPLICATION NUMBER: US/09/932,165

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/226,329

; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 1508

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 284

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

; US-09-932-165-284

; Query Match

56.2%; Score 31.5;

DB 10; Length 9;

; Best Local Similarity 60.0%; Pred. No. 1.2e+06;

; Matches 6; Conservative 2; Mismatches 2;

; Indels 1; Gaps 1;

; TYPE: PRT

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

; US-09-932-165-284

; Query Match

56.2%; Score 31.5;

DB 10; Length 10;

; Best Local Similarity 60.0%; Pred. No. 1.6e+02;

; Matches 6; Conservative 2; Mismatches 1;

; Indels 1; Gaps 1;

; Query

1 CISVPLSVPC 10

1 CLT-PLSFP'C 9

; Db

; RESULT 11

US-09-932-165-184

; Sequence 184, Application US/09932165

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: PARIS, MARY

; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBIVITS, AYA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND

; TITLE OF INVENTION: DETECTION OF CANCER

; FILE REFERENCE: 51158-20014.00

; CURRENT APPLICATION NUMBER: US/09/932,165

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/226,329

; NUMBER OF SEQ ID NOS: 1508

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 184

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; ;

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

; US-09-932-165-184

; Query Match

56.2%; Score 31.5;

DB 10; Length 10;

; Best Local Similarity 60.0%; Pred. No. 1.6e+02;

; Matches 6; Conservative 2; Mismatches 1;

; Indels 1; Gaps 1;

; Query

1 CISVPLSVPC 10

1 CLT-PLSFP'C 9

; Db

; RESULT 12

US-09-932-165-560

; Sequence 560, Application US/09932165

; Publication No. US20030134784A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: PARIS, MARY

; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBIVITS, AYA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND

; TITLE OF INVENTION: DETECTION OF CANCER

; FILE REFERENCE: 51158-20014.00

; CURRENT APPLICATION NUMBER: US/09/932,165

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/226,329

; NUMBER OF SEQ ID NOS: 1508

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 560

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; ;

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

; US-09-932-165-560

; Query Match

56.2%; Score 31.5;

DB 10; Length 10;

; Best Local Similarity 60.0%; Pred. No. 1.6e+02;

; Matches 6; Conservative 2; Mismatches 1;

; Indels 1; Gaps 1;

; Query

1 CISVPLSVPC 10

1 CLT-PLSFP'C 9

; Db

; RESULT 13

US-09-932-165-794

; Sequence 794, Application US/09932165

; Publication No. US20030134784A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: PARIS, MARY

; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBIVITS, AYA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND

; TITLE OF INVENTION: DETECTION OF CANCER

; FILE REFERENCE: 51158-20014.00

; CURRENT APPLICATION NUMBER: US/09/932,165

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/226,329

; NUMBER OF SEQ ID NOS: 1508

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 184

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; ;

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; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-794          RESULT 15
                                ; Sequence 194, Application US/10363791
                                ; Publication No. US20040029197A1
                                ; GENERAL INFORMATION:
                                ; APPLICANT: TAKIMOTO, Masato
                                ; APPLICANT: KUZUMAKI, No. US20040029197A1oru
                                ; APPLICANT: SATO, No. US20040029197A1iyuki
                                ; APPLICANT: SAHARA, Hirceki
                                ; TITLE OF INVENTION: A novel human cancer/testis-associated gene thereof
                                ; FILE REFERENCE: 4439-A006
                                ; CURRENT APPLICATION NUMBER: US/10/363-791
                                ; CURRENT FILING DATE: 2003-03-07
                                ; PRIOR APPLICATION NUMBER: US/2000-274218
                                ; PRIOR FILING DATE: 2000-09-08
                                ; NUMBER OF SEQ ID NOS: 227
                                ; SOFTWARE: PatentIn version 3.2
                                ; SEQ ID NO 194
                                ; LENGTH: 10
                                ; TYPE: PRT
                                ; ORGANISM: Homo sapiens
US-10-363-791-194          Query Match      56.2%; Score 31.5; DB 10; Length 10;
                                ; Best Local Similarity 60.0%; Pred. No. 1.6e+02;
                                ; Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
                                ; Qy          1 CCSVPLSYPC 10
                                ; Db          1 :|:|||:|
                                ; CTT-PLSFPC 9
                                ; LENGTH: 10
                                ; TYPE: PRT
                                ; ORGANISM: Homo sapiens
US-10-363-791-194          Query Match      55.4%; Score 31; DB 12; Length 10;
                                ; Best Local Similarity 83.3%; Pred. No. 1.9e+02;
                                ; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
                                ; Qy          5 PLSVPC 10
                                ; Db          2 ||| |
                                ; PLASAPC 7
                                ; LENGTH: 10
                                ; TYPE: PRT
                                ; ORGANISM: Homo sapiens
US-10-363-791-194          Search completed: September 5, 2004, 11:40:12
                                ; Job time : 67 secs

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; PRIOR APPLICATION NUMBER: US/10/154,884B
; CURRENT APPLICATION NUMBER: US/10/154,884B
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 01/4058-013521US
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; SEQ ID NO 11290
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11221
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11221        Query Match      55.4%; Score 31; DB 15; Length 9;
                                ; Best Local Similarity 71.4%; Pred. No. 1.2e+06;
                                ; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
                                ; Qy          1 CCSVPLS 7
                                ; Db          2 ||| |
                                ; CLSVPVPS 8

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GenCore version 5.1.6
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OM protein - protein search, using sw mode.

Run on: September 5, 2004, 11:32:18 ; search time 15 seconds
(without alignments)
34,417 Million cell updates/sec

Title: US-09-761-636A-13
Perfect score: 56
Sequence: 1 CISVELSVPVC 10

Scoring table: BLOSUM62
Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 103740

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries:

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 3: /cgn2_6_ptodata/2/iaa/6A_COMB.pep:
 4: /cgn2_6_ptodata/2/iaa/6B_COMB.pep:
 5: /cgn2_6_ptodata/2/iaa/PCTUS_COMB.pep:
 6: /cgn2_6_ptodata/2/iaa/backfiles_COMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB ID	Description
1	3.6	64.3	9	1	US-08-331-383-33
2	3.6	64.3	9	1	US-08-549-008-43
3	3.6	64.3	9	3	US-08-981-143
4	3.3	58.9	9	1	US-08-331-383-31
5	3.3	58.9	9	1	US-08-549-008-42
6	3.3	58.9	9	3	US-08-802-981-142
7	2.5	44.6	10	1	US-08-212-190A-5
8	2.5	44.6	10	2	US-08-900-321-5
9	2.5	44.6	10	3	US-09-451-697-21
10	2.5	44.6	10	5	PCT-US95-03610-5
11	2.4	42.9	6	1	US-08-483-43A-21
12	2.4	42.9	6	3	US-08-476-13A-30
13	2.4	42.9	6	6	5120920-26
14	2.4	42.9	6	6	5506208-28
15	2.4	42.9	9	1	US-08-331-383-35
16	2.4	42.9	9	1	US-08-549-008-40
17	2.4	42.9	9	3	US-08-802-981-1
18	2.4	42.9	10	1	US-08-033-857A-5
19	2.4	42.9	10	1	US-08-374-982A-5
20	2.4	42.9	10	3	US-08-377-78A-17
21	2.3	41.1	6	1	US-07-994-133-3
22	2.3	41.1	6	1	US-08-221-07A-8
23	2.3	41.1	6	1	US-08-221-17A-8
24	2.3	41.1	8	1	US-08-189-331-147
25	2.3	41.1	8	1	US-08-189-331-148
26	2.3	41.1	8	1	US-08-189-331-149
27	2.3	41.1	8	1	US-08-189-331-150

ALIGNMENTS

RESULT 1
US-08-331-383-33
; Sequence 33, Appl. Application US/08331383
; Patent No. 5605809
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; ADDRESS: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; Proteases in Biological Samples and Methods and Use
; TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Parent-In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,383
; FILING DATE: 28-OCT-1994
; CLASIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEX/FAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-383-33
Query Match 64.3%; Score 36; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indexes 0; Gaps 0;
Qy 3 SVPLSYPC 10
Db 2 AIPMS:PC 9

RESULT 2
US-08-549-008-43
Sequence 143, Application US/08549008
GENERAL INFORMATION:
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,008
FILING DATE: 27-OCT-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/331,383
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 3,2,762
REFERENCE/DOCKET NUMBER: 016865-000110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-549-008-43

Query Match 64.3%; Score 36; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLSYPC 10
DB 2 AIPMSIPC 9

RESULT 4
US-08-331-383-31
Sequence 31, Application US/08331383
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,383
FILING DATE: 28-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 16865-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single

RESULT 3
US-08-802-981-143
Sequence 143, Application US/08802981
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Region
 LOCATION: one-of{(5)
 OTHER INFORMATION: /note= "Xaa is norleucine."
 US-08-331-333-31

Query Match 58.9%; Score 33; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 3e+05; 3; Mismatches 1; Indels 0; Gaps 0;
 Matches 4; Conservative 4; Number of SEQUENCES: 231

Qy 3 SVPLSVPc 10
 Db 2 AIPXSIPC 9

RESULT 5
 US-08-549-008-42
 Sequence 42, Application US/08549008
 Patent No. 5714342

GENERAL INFORMATION:
 APPLICANT: Komoriya, Akira
 ADDRESS: Packard, Beverly S.
 TITLE OF INVENTION: Compositions for the Detection of Enzyme
 NUMBER OF SEQUENCES: 56

Query Match 58.9%; Score 33; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 3e+05; 3; Mismatches 1; Indels 0; Gaps 0;
 Matches 4; Conservative 4; Number of SEQUENCES: 231

Qy 3 SVPLSVPc 10
 Db 2 AIPXSIPC 9

RESULT 6
 US-08-802-981-142
 Sequence 142, Application US/08802981
 Patent No. 6037137

GENERAL INFORMATION:
 APPLICANT: Komoriya, Akira
 ADDRESS: Packard, Beverly S.
 TITLE OF INVENTION: Compositions for the Detection of Enzyme
 NUMBER OF SEQUENCES: 231

Query Match 58.9%; Score 33; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 3e+05; 3; Mismatches 1; Indels 0; Gaps 0;
 Matches 4; Conservative 4; Number of SEQUENCES: 231

Qy 3 SVPLSVPc 10
 Db 2 AIPXSIPC 9

RESULT 7
 US-08-212-190A-5
 Sequence 5, Application US/08212190A
 Patent No. 5652223

GENERAL INFORMATION:
 APPLICANT: LICHTA, Lance A.
 ADDRESS: KIM, Young Sook
 TITLE OF INVENTION: DNA ENCODING CA1 RESISTANCE PROTEINS AND
 NUMBER OF SEQUENCES: 10

Query Match 58.9%; Score 33; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 3e+05; 3; Mismatches 1; Indels 0; Gaps 0;
 Matches 4; Conservative 4; Number of SEQUENCES: 42

Qy 3 SVPLSVPc 10
 Db 2 AIPXSIPC 9

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COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,190A
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 435
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15280-204US
REFERENCE/DOCKET NUMBER: DHHS Ref. No. 5652223 E-112-94/0
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: peptide
MOLECULE TYPE: peptide
US-08-212-190A-5

Query Match 44.6%; Score 25; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
US-08-900-321-5
; Sequence 5, Application US/08900321
; Patent No. 5881712
; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Kim, Young S.
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-1834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; APPLICATION NUMBER: US 08/212,190

Query Match 44.6%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 9
US-09-461-697-21
; Sequence 21, Application US/09461697
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Puranam, Kasturi
; APPLICANT: Porbury, Stuart D.
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: AND TREATING CONDITIONS,
; TITLE OF INVENTION: CELL DEATH
; TITLE OF INVENTION: CELL DEATH
; CURRENT APPLICATION NUMBER: US/09/461,697
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-697-21

Query Match 44.6%; Score 25; DB 3; Length 10;
Best Local Similarity 44.4%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 10
PCT-US95-03610-5
; Sequence 5, Application PC/TUS9503610
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; APPLICATION NUMBER: US 08/212,190

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FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31-677
REFERENCE/DOCKET NUMBER: 15280-204000PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-03610-5

Query          Score 25; DB 5; Length 10
Best Local Similarity 66.7%; Prod. No. 2.7e+02;
Matches        4; Conservative 0; Mismatches 2; Indels
      5 PLSVPC 10
      5 PAPVPC 8
      3 PAPVPC 8

RESULT 11
US-08-483-434A-21
Sequence 21, Application US/08483434A
Patent No. 5618461
GENERAL INFORMATION:
APPLICANT: EVAL, Jacob
APPLICANT: HAMILTON, Bruce K.
APPLICANT: TUSZYNSKI, George P.
TITLE OF INVENTION: Synthetic Analogs of Thrombospondin
TITLE OF INVENTION: Therapeutic Use Thereof
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,434A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/450,738
FILING DATE: 25-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/185,614
FILING DATE: 24-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,436
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/587,197
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/483,527
FILING DATE: 22-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-3UUS (9049)

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; TELECOMMUNICATION INFORMATION
; TELEPHONE: (215) 567-2020
; TELEX: (215) 567-2991
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-483-434A-21

Query Match          42.9%; S
Best Local Similarity 100.0%; I
Matches 4; Conservative 0;
Qy      7 SVPC 10
Db      2 SVPC 5

RESULT 12
US-08-476-134A-30
; Sequence 30, Application US/08476
; Patent No. 6239110
; GENERAL INFORMATION:
; APPLICANT: EYAL, JACOB
; APPLICANT: HAMILTON, BRUCE K.
; APPLICANT: TUZYNSKI, GEORGE P.
; TITLE OF INVENTION: SYNTHETIC P.
; TITLE INVENTION: THEREOF
; FILE REFERENCE: 07206-0609
; CURRENT APPLICATION NUMBER: US/01
; CURRENT FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/58
; PRIOR FILING DATE: 1990-09-24
; PRIOR APPLICATION NUMBER: 07/48
; PRIOR FILING DATE: 1990-02-22
; PRIOR APPLICATION NUMBER: 08/45
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/18
; PRIOR FILING DATE: 1994-01-24
; PRIOR APPLICATION NUMBER: 08/02
; PRIOR FILING DATE: 1993-03-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of
; OTHER INFORMATION: analog of the
US-08-476-134A-30

Query Match          42.9%; S
Best Local Similarity 100.0%; I
Matches 4; Conservative 0;
Qy      7 SVPC 10
Db      2 SVPC 5

RESULT 13
5190920-26
; Patent No. 5190920
; APPLICANT: EYAL, JACOB; HAMILTON
; GEORGE P.
; TITLE OF INVENTION: METHOD FOR
; OF THROMBOSPONDIN FOR INHIBITING ME
; HAMPTON, C.
; OTHER INFORMATION: 2000-01-26

```

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/587,197
 ; FILING DATE: 24-SEP-1990
 ; SEQ ID NO:26;
 ; LENGTH: 6
 5509020-26

Query Match 42.9%; Score 24; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 7 SVPC 10
 Db 2 SVPC 5

RESULT 14
 5506208-28
 ; Patent No. 5506208
 ; APPLICANT: EYAL, JACOB ; HAMILTON, BRUCE K. ; TUSZYNSKI,
 ; GEORGE P.
 ; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF
 ; THROMBOPONDIN FOR INHIBITING ANGIOGENESIS ACTIVITY
 ; NUMBER OF SEQUENCES: 45
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/408,181
 ; FILING DATE: 22-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 131,565
 ; FILING DATE: 04-OCT-1993
 ; APPLICATION NUMBER: 895,764
 ; FILING DATE: 09-JUN-1992
 ; APPLICATION NUMBER: 587,197
 ; FILING DATE: 24-SEP-1990
 ; SEQ ID NO:28;
 ; LENGTH: 6
 5506208-28

Query Match 42.9%; Score 24; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 7 SVPC 10
 Db 2 SVPC 5

RESULT 15
 US-08-331-3-83-35
 ; Sequence 35, Application US/08331383
 ; Patent No. 5605809

GENERAL INFORMATION:
 ; APPLICANT: Komariya, Akira
 ; APPLICANT: Packard, Beverly S.
 ; TITLE OF INVENTION: Compositions for the Detection of
 ; Proteases in Biological Samples and Methods and Use
 ; TITLE OF INVENTION: Thereof
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Stewart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/331,383
 ; FILING DATE: 28-OCT-1994

GenCore version 5.1.6
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file: perfect score: US-09-761-636A-14
52

Scoring table: BLOSUM62

searched: 283366 seqs, 96191526 residues

maximum DB seq length: 9

Maximum Match 100%
Listing First 45 su

base : PIR_78:*

part 3: * 1

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SISTEMAS DE

The Query Rule

				MHC H2-L antigen -
1	22	42.3	6	165516
2	2	19	5	2 A60521
3	3	19	36.5	9 2 A60356
4	4	18	34.6	9 2 A61620
5	5	17	32.7	8 2 S10783
6	6	17	32.7	9 2 S66419
7	7	16	30.8	4 2 I51049
8	8	16	30.8	9 2 S13636
9	9	15	28.8	6 2 H48334
10	10	15	28.8	8 2 G33038
11	11	15	28.8	8 4 I54017
12	12	15	28.8	9 2 PT0000
13	13	14	26.9	7 2 I48115
14	14	14	26.9	8 2 S21288
15	15	14	26.9	9 2 D48186
16	16	14	26.9	9 2 PH0943
17	17	13	25.0	5 2 E42364
18	18	13	25.0	7 2 S42620
19	19	13	25.0	8 2 B39745
20	20	13	25.0	8 2 A42659
21	21	13	25.0	9 2 B28435
22	22	13	25.0	9 2 PT0247
23	23	13	25.0	9 2 PT0268
24	24	13	25.0	9 2 S26508
25	25	12	23.1	5 2 B22555
26	26	12	23.1	6 2 B34835
27	27	12	23.1	6 2 B26206
28	28	12	23.1	6 4 A35039
29	29	12	23.1	7 2 ECMTTR

seed Protein ws-5		Ig H chain V-D-J r	
		T-cell receptor be	hypothetical prote
0	E61491	neutral proteinase	T-cell receptor be
1	23.1	PH1602	sperm-activating p
1	23.1	7	kidney and bladder
1	23.1	7	phosphoenolpyruvate
2	23.1	PH0912	3', 5'-cyclic-GMP p
2	23.1	7	T-cell receptor be
3	23.1	S16324	T-cell receptor be
3	23.1	8	T-cell receptor be
4	23.1	A35180	T-cell receptor be
4	23.1	8	T-cell receptor be
5	23.1	PH0914	T-cell receptor be
5	23.1	8	T-cell receptor be
6	23.1	S19229	T-cell receptor be
6	23.1	9	T-cell receptor be
7	23.1	G58902	T-cell receptor be
7	23.1	9	T-cell receptor be
8	23.1	S55616	T-cell receptor be
8	23.1	9	T-cell receptor be
9	23.1	A53777	T-cell receptor be
9	23.1	9	T-cell receptor be
0	23.1	PH0935	T-cell receptor be
0	23.1	9	T-cell receptor be
1	23.1	PH0917	T-cell receptor be
1	23.1	9	T-cell receptor be
2	23.1	PH0912	T-cell receptor be
2	23.1	9	T-cell receptor be
3	23.1	PH0917	T-cell receptor be
3	23.1	9	T-cell receptor be
4	23.1	PH0918	T-cell receptor be
4	23.1	9	T-cell receptor be
5	23.1	PH0921	T-cell receptor be
5	23.1	9	T-cell receptor be
6	23.1	PH0922	T-cell receptor be
6	23.1	9	T-cell receptor be
7	23.1	PH0923	T-cell receptor be
7	23.1	9	T-cell receptor be
8	23.1	PH0924	T-cell receptor be
8	23.1	9	T-cell receptor be
9	23.1	PH0925	T-cell receptor be
9	23.1	9	T-cell receptor be
10	23.1	PH0926	T-cell receptor be
10	23.1	9	T-cell receptor be
11	23.1	PH0927	T-cell receptor be
11	23.1	9	T-cell receptor be
12	23.1	PH0928	T-cell receptor be
12	23.1	9	T-cell receptor be

ALIGNMENTS

RESULT 1

165546 MHC H-2_L antigen - mouse - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C;Accession: I65546
 R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
 Cell 44, 261-272, 1986
 A;Title: Detailed analysis of the mouse H-2_{Kb} promoter: Enhancer-like sequence
 A;Reference number: 152778; MUID:86106202; PMID:3510743
 A;Accession: I65546
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-6 <RES>
 A;Cross References: GB:MM12483; NID:gi199565; PIDN:AAA99663.1; PID:g554234

Qy	6 LIVPC 9	Score	22;	DB	2;	Length	6;
Db	:	Pred.	No.	2.8e+05;			
	1 MVPC 4	Matches	3;	Conservative	1;	Mismatches	0;
						Indels	0;
						Gaps	0

RESULT 2

A60521 Glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
 N;Alternate names: glycogen phosphorylase b
 C;Species: Liza ramada
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
 C;Accession: A60521
 R;Bonamusa, L.; Baanante, I.V.
 Comp. Biochem. Physiol. B 95, 295-301, 1990
 A;Title: Purification and characterization of glycogen phosphorylase B from skates
 A;Reference number: A60521; MUID:90227907; PMID:2109669
 A;Accession: A60521
 A;Molecule type: protein
 A;Residues: 1-5 <BON>
 C;Superfamily: glucan phosphorylase
 C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
 F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #statistic

Qy	2 ISVP 5	Score	19;	DB	2;	Length	5;
Db	:	Pred.	No.	2.8e+05;			
	2 ISVP 5	Matches	4;	Conservative	0;	Mismatches	0;
						Indels	0;
						Gaps	0

RESULT 3
 A60356
 11KX stomach cancer antigen - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
 C;Accession: A60356
 R;Shiraishi, Y.
 Int. J. Cancer 45, 783-787, 1990
 A;Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens by
 A;Reference number: A60356; MUID:90216080; PMID:2323853
 A;Molecule type: protein
 A;Residues: 1-9 <SHI>
 C;Keywords: glycoprotein

Query Match 36.5%; Score 19; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VPLVP 8
 Db 1 IPLKP 5

RESULT 4
 A61620
 Locustambyotropin III - migratory locust
 C;Species: Locusta migratoria (migratory locust)
 C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
 C;Accession: A61620
 R;Schools, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
 Insect Biochem. Mol. Biol. 22, 441-452, 1992
 A;Title: Isolation, identification and synthesis of locustambyotropin III and IV, two add
 A;Reference number: A61620
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <SCH>
 C;Keywords: amidated carboxyl end; neuropeptide F;
 F;Modified site: amidated carboxyl end (Ieu) #status experimental

Query Match 34.6%; Score 18; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PLVP 8
 Db 4 PFVP 7

RESULT 5
 S10783
 enamelin f - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
 C;Accession: S10783
 R;Strawich, E.; Glimcher, M.J.
 Eur. J. Biochem. 191, 47-56, 1990
 A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is also
 A;Reference number: S10780; MUID:90336641; PMID:2379503
 A;Accession: S10783
 A;Molecule type: protein
 A;Residues: 1-8 <STR>
 C;Keywords: enamel; phosphoprotein

Query Match 32.7%; Score 17; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VPLVP 8
 Db 1 MPLPP 5

RESULT 6
 S66419
 tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)
 C;Species: Spinacia oleracea (spinach)
 C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997
 C;Accession: S66419
 R;Ruwabara, T.
 PESS Lett. 371, 195-198, 1995
 A;Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spinach
 A;Reference number: S66419; MUID:95402209; PMID:7672127
 A;Accession: S66419
 A;Molecule type: protein
 A;Residues: 1-9 <RDW>

Query Match 32.7%; Score 17; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLVP 8
 Db 2 PILP 5

RESULT 7
 I51049
 metallothionein-A - rainbow trout (fragment)
 C;Species: Oncorhynchus mykiss (rainbow trout)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C;Accession: I51049
 R;Olsson, P.E.; King, P.J.; Kille, P.
 Eur. J. Biochem. 230, 344-349, 1995
 A;Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) metallothionein-A. Reference number: I51049; MUID:95324545; PMID:7601121
 A;Accession: I51049
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Cross-references: EMBL:X80181; NID:91019799; PID:CAA56466.1; PID:94379328
 A;Residues: 1-4 <COLS>

Query Match 30.8%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PC 9
 Db 3 PC 4

RESULT 8
 S13636
 coat protein beta chain, Golgi-derived - rabbit (fragment)
 N;Alternative names: beta COP protein
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
 C;Accession: S13636
 R;Serafini, T.; Stanbeck, G.; Brecht, A.; Lottspeich, F.; Orci, L.; Rothman, J.E.; Wieland, Nature 349, 215-220, 1991
 A;Title: A coat subunit of Golgi-derived non-clathrin-coated vesicles with homology to trans-Golgi apparatus
 A;Reference number: S13636; MUID:9101693; PMID:1898984
 A;Accession: S13636
 A;Molecule type: protein
 A;Residues: 1-9 <SSR>
 C;Superfamily: coatomer complex beta chain
 C;Keywords: Golgi apparatus; protein transport

Query Match 30.8%; Score 16; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VPLVP 7
 Db 5 IPIV 8

RESULT 9
 H43394 glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
 C;Accession: H43394 R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
 Biochem. Mol. Biol. Int. 29, 545-554, 1993
 A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.
 A;Reference number: MUID:93250576; PMID:8485470
 A;Accession: H43394; MUID:93250576; PMID:8485470
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-6 <MAT>
 A;Experimental source: milk
 A;Note: sequence extracted from NCBI backbone (NCBIP:131518)
 C;Keywords: glycoprotein

Query Match Score 15; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VPLVPC 9
 Db 1 VELIGC 6

RESULT 10
 G33098 205K exoantigen - malaria parasite (*Plasmodium falciparum*) (fragments)
 C;Species: Plasmodium falciparum
 C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C;Accession: G33098 R;Nichols, J.H.; Hager, L.P.
 Submitted to the Protein Sequence Database, May 1990
 A;Reference number: A33098
 A;Accession: G33098
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-8 <NIC>

Query Match Score 15; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VPL 6
 Db 2 VPL 4

RESULT 11
 I54017 granulocyte-colony stimulating factor precursor - synthetic (fragment)
 C;Species: synthetic
 A;Note: human gene engineered and expressed in *Escherichia coli*
 C;Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
 C;Accession: I54017 R;Devin, P.B.; Drummond, R.J.; Toy, P.; Mark, D.F.; Watt, K.W.; Devlin, J.J.
 Gene 65, 13-22, 1988
 A;Title: Alteration of amino-terminal codons of human granulocyte-colony-stimulating fact.
 A;Reference number: I54017; MUID:88284374; PMID:2456256
 A;Accession: I54017
 A;Status: translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-8 <DEV>
 A;Cross-references: GB:M20922; MUID:9806638; PMID:AAA6653.1; PID:9183043

Query Match Score 15; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Query Match 26.9%; Score 14; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 3;

```

QY          3 VPLVP 8
          | |
          3 STPSPP 8
Db

```

RESULT 15

D48186
 ATPase R1 subunit - wood tobacco (fragment)
 C;Species: Nicotiana sylvestris (wood tobacco)
 C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
 C;Accession: D48186
 R;De Paep, R.; Forchioni, A.; Chetrit, P.; Vedel, F.
 Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
 A;Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase
 A;Reference number: A48186; MUID:33317598; PMID:8327163
 A;Accession: D4186
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 1-9
 A;Experimental source: Pollen
 A;Note: sequence extracted from NCBI backbone (NCBIP:134871)

Query Match 26.9%; Score 14; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 2;

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QY          4 VPLVP 8
          | |
          3 VDLAP 7
Db

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Search completed: September 5, 2004, 11:06:22
 Job time : 11.6667 secs

Scoring table:	BLOSUM62	
	Gapop 10.0 , Gapext 0.5	
Searched:	141681 seqs, 52070155 residues	
Total number of hits satisfying chosen parameters:	251	
Minimum DB seq length:	0	
Maximum DB seq length:	9	
Post-processing:	Minimum Match 0% Maximum Match 100%	
	Listing First 45 summaries	
Database :	SwissProt_42: [*]	
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
	SUMMARIES	
Result No.	Score	Query Match Length DB ID Description
1	20	38.5 9 1 MGMT_BOVIN
2	18	34.6 8 1 COM2_CONPU
3	18	34.6 9 1 LMT3_LOCOMI
4	17	32.7 9 1 UPB3_HUMAN
5	16	30.8 8 1 PPK2_PERAM
6	15	28.8 8 1 PPK3_PERAM
7	13	28.8 9 1 UPB7_HUMAN
8	13	25.0 6 1 E101_LITRU
9	13	25.0 9 1 CONO_CONST
10	12	23.1 7 1 CARP_MYTED
11	12	23.1 8 1 ALL6_CVDPO
12	12	23.1 8 1 FUS5_FUSSO
13	12	23.1 8 1 UPB1_HUMAN
14	12	23.1 9 1 FAR5_PERMO
15	12	23.1 9 1 FLA2_TREHY
16	12	23.1 9 1 OXYT_BUFR
17	12	23.1 9 1 SAP_STOVA
18	11	21.2 6 1 VP19_HSV1
19	11	21.2 7 1 CCP1_ENTFA
20	11	21.2 7 1 MNPI_LBEDE
21	11	21.2 7 1 TPFY_PACDA
22	11	21.2 8 1 VGEIG_HSV2B
23	11	21.2 9 1 COX6_THROB
24	11	21.2 9 1 DNPI_LOCOMI
25	11	21.2 9 1 FAR9_ASCSSU
26	11	21.2 9 1 OXVA_SQUAC
27	11	21.2 9 1 OXYT_RABIT
28	11	21.2 9 1 PTC3_BOVIN
29	10	19.2 7 1 TYS1_LITRU
30	10	19.2 7 1 UFG4_MOUSE
31	10	19.2 9 1 COW_COVNE
32	10	19.2 9 1 PPK1_PERAM
33	10	19.2 9 1 TAII_PICJA
	ALIGNMENTS	
RESULT 1		
MGMT_BOVIN		
ID MGMT_BOVIN		
AC P29177;		
DT 01-DEC-1992 (Rel. 24, Created)		
DT 01-DEC-1992 (Rel. 24, Last sequence update)		
DT 01-OCT-1996 (Rel. 34, Last annotation update)		
DE Methylated-DNA--protein-cysteine methyltransferase (BC 2.1.1.63) (6-O-methyl-L-guanine-DNA methyltransferase) (Fragment).		
GN MGMT.		
OS Bos taurus (Bovine).		
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae; Bovinae; Bos.		
OC NCBI_TaxID=9913;		
RN [1] ;		
RP SEQUENCE.		
RC TISSUE=Thymus;		
RC MEDLNB=90174912; PubMed=2308822;		
RA Rydberg B.; Hall J.; Karren P.;		
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA methyltransferase".		
RL Nucleic Acids Res. 18:17-21(1990).		
CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the O-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is irreversibly inactivated.		
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein S-methyl-L-cysteine.		
CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.		
CC DR InterPro: IPR01497; Methytransfer_1.		
DR PROSITE: PS00374; MGMT; PARTIAL.		
KW DNA repair; Transferase; Methyltransferase.		
FT NON_TER	1	
FT ACT SITE	9	
FT NON_TER	9	
SEQUENCE 9 AA: 967 MN; 325171A/20476047 CRC64;		
Query Match 38.5%; Score 20; DB 1; Length 9;		
Best Local Similarity 75.0%; Pred. No. 1.4e+05;		
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy 6 LVPC 9		
Db 6 LTPC 9		
RESULT 2		
COW2_CONPU		
ID COW2_CONPU		
AC P58755;		
DT 28-FEB-2003 (Rel. 41, Created)		
DT 28-FEB-2003 (Rel. 41, Last sequence update)		
DT 28-FEB-2003 (Rel. 41, Last annotation update)		

DE Leu-contryphan-P.

OS Conus purpurascens (Purple cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=41690;

RN [1]

RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

RC STRAIN=Clipperton Island; TISSUE=venom;

RX MEDLINE=9938839; PubMed=10461743;

RA Jacobson R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,

RA Olivera B.M.;

RT "A novel D-leucine-containing Conus peptide: diverse conformational

RT dynamics in the contryphan family.";

RL Pept. Res. 54:93-99 (1999).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.

CC -!- SIMILARITY: Belongs to the contryphan family.

KW Toxin; Hydroxylation; D-amino acid.

FT DISULFID 2 8

FT MOD RES 4 4 D-LEUCINE.

FT SQ 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 34.6%; Score 18; DB 1; Length 8;

Best Local Similarity 40.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVP 5

Db 2 CVLPP 6

RESULT 3

LMT3 LOCMI STANDARD; PRT; 9 AA.

AC P41489;

ID LMT3 LOCMI STANDARD; PRT; 9 AA.

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Orthopteroidea; Orthoptera; Caelifera; Acrideromorpha; Acridoidea; Acriidae; Oedipodinae; Locusta.

NCBI_TaxID=7004;

OX [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Brain;

RA de Loof A.;

RT "Isolation, identification and synthesis of locustamotropin III and IV, two additional neuropeptides of *Locusta migratoria*: members of the locustamotropin peptide family.";

RT Insect Biochem. Mol. Biol. 22:447-452(1992).

CC -!- FUNCTION: Potent mediator of visceral muscle contractile activity

CC -!- SIMILARITY: Belongs to the pyrokinin family.

PIR; A61620; A61620.

DR InterPro; IPR001484; Pyrokinin.

DR PROSITE; PS00539; PYROKININ; 1.

KW Neuopeptide; Amidation; Pyrokinin.

FT MOD RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C CRC64;

Query Match 34.6%; Score 18; DB 1; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVP 8

Db 4 PRFP 7

RESULT 4

UPA3_HUMAN STANDARD; PRT; 9 AA.

ID UPA3_HUMAN AC P30089;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).

OS Homo sapiens (Human).

OC Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

OX [1]

RN RP SEQUENCE,

RC TISSUE=Plasma;

RX MEDLINE=93092937; PubMed=1459097;

RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C., Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B., Hochstrasser D.F.;

RT "Plasma protein map: an update by microsequencing.";

RL Electrophoresis 13:707-714 (1992).

CC -!- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown protein is 4.6, its MW is: 46 kDa.

DR SWISS-2DPAGE; P30089; HUMAN.

FT NON_TER 1 1

SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 32.7%; Score 17; DB 1; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVP 8

Db 2 PLFP 5

RESULT 5

PPK2_PEPAM STANDARD; PRT; 8 AA.

ID PPK2_PEPAM AC P86692;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pyrokinin-2 (Pea-PK-2) (FXPLI-amide).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.

NCBI_TaxID=6978;

OX [1]

RN RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Corpora cardiaca;

RX MEDLINE=27353923; PubMed=9210163;

RA Prede R., Kallner R., Kaufmann R., Penzlin H., Gaede G.; RT "Isolation and structural elucidation of two pyrokinins from the retrocerebral complex of the American cockroach.";

RT Peptides 18:473-478 (1997).

RL RN RP TISSUE SPICIFICITY. PubMed=10723010;

RA Prede R., Eckert M.; RT "Tissue-specific distribution of FXPRLamides in the nervous system of the American cockroach";

RL J. Comp. Neurol. 419:352-363 (2000).

CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic activity);

CC -!- TISSUE SPECIFICITY: Corpora cardiaca.

CC -!- MASS SPECTROMETRY: MW=883; METHOD=VALDI.

CC -!- SIMILARITY: Belongs to the pyrokinin family.

DR InterPro; IPR001484; Pyrokinin.

DR PROSITE; PS00539; PYROKININ; 1.

DR PROSITE; PS00539; PYROKININ; FALSE_NEG.

KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD-RES 8 B
 SQ SEQUENCE 8 AA; 884 MW; C834176DD77775 CRC64;

Query Match 30.0%; Score 16; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 SYPLVP 8
 Db 1 SPFFPAP 6

RESULT 6
 PPK3 PERAM STANDARD PRT; 8 AA.

ID PPK3 PERAM
 AC P82618;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 Blattidae; Periplaneta.
 OC NCBI_TaxID=6974;
 RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE-Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Different distribution of pyrokinin isoforms in cerebral and abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144 (1999).
 RN [2]

RP TISSUE SPECIFICITY.
 RX MEDLINE=20188984; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tissue-specific distribution of FXPRlamides in the nervous system of the American cockroach.";
 RL J. Comp. Neurol. 419:352-363 (2000).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic activity).
 CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
 CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.

KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD-RES 8 B
 SQ SEQUENCE 8 AA; 997 MW; 0B341740D772C7 CRC64;

Query Match 28.0%; Score 15; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LVP 8
 Db 1 LVP 3

RESULT 7
 UPA7 HUMAN STANDARD PRT; 9 AA.

ID UPA7 HUMAN
 AC P30093;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DB Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE.

RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C., Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B., Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing."
 RL Electrophoresis 13:707-714 (1992).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is 5.05, its MW is: 37 kDa.
 DR SWISS-2DPAGE; P30093; HUMAN.
 FT NON-TER 1 1
 FT UNSURE 5 5
 FT NON-TER 9 9
 SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;

RESULT 8
 BI01_LITTRU STANDARD PRT;
 ID BI01_LITTRU
 AC P82096;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Electrin 1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chorata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Pelodytadinae; Litoria.
 OC NCBI_TaxID=104895;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog Litoria electrin 1.";
 RL Aust. J. Chem. 52:639-645 (1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense peptide; Amidation.
 FT MOD-RES 6 6
 SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 25.0%; Score 13; DB 1; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VPL 6
 Db 2 VPI 4

RESULT 9
 CONO_CONST STANDARD PRT;
 ID CONO_CONST
 AC P05487;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Arg-conopeptins S.
 OS Conus striatus (Striated cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Sorbeoconcha; Hypsogastropoda; Apogastropoda; Caenidea; Conidae; Conus.
 OC NCBI_TaxID=6493;

RN
RP
SEQUENCE; PubMed=3560228;
RX MEDLINE=88056932; PubMed=3560228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
peptides from Conus geographus and Conus straitus venoms.";
RT J. Biol. Chem. 262:15821-15824 (1987).
RN
RP
REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus "snails.";
Ann. Rev. Biochem. 57:665-700 (1988).
CC
-!- FUNCTION: Targets vasopressin/oxytocin related receptors.
CC
-!- SUBCELLULAR LOCATION: Secreted.
CC
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC
-!- SIMILARITY: Belongs to the vasoressin/oxytocin family.
PIR; B28495; B28495.
DR InterPro IPR000981; Neurohyp_horm.
DR Pfam PF00220; hormone4_1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISTFLD 1 6 AMIDATION.
MOD RES 9 9 AMIDATION.
SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;
Query Match 25.0%; Score 13; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CI 2
Db 1 CI 2

RESULT 10
CARP_MYTED STANDARD; PRT; 7 AA.
ID CARP_MYTED
AC P10470;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DB Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Bivalvia; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
OC Mytilidae; Mytilidae; Mytilus.
RN
RP
SEQUENCE; PubMed=38052022; PubMed=3676797;
RX MEDLINE=88056932; PubMed=3560228;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Munsoo Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC
-!- FUNCTION: This peptide exhibits both potentiating (contraction)
and inhibitory (relaxation) effects on the anterior byssus
retractor muscle.
DR PIR; A29342; BCMUCR.
KW Hormone; Amidation.
MOD RES 7 AMIDATION.
SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 23.1%; Score 12; DB 1; Length 7;
Best Local Similarity 20.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 3 SVPLV 7
Db 1 AMPML 5

RESULT 11
CYPDPO STANDARD; PRT; 8 AA.
ID ALI6_CYPDPO
AC P8157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DB Cyiaastatin 6.
OS Cyia pomonella (Codling moth).
OC Eukaryota; Metazoa; Anthropterygota; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Gloissata; Ditrysia;
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
NCBI_TaxID=82600;
RN
RP
SEQUENCE.
RC TISSUE=larva;
MEDLINE=9805539; PubMed=9392829;
RA Dure H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309 (1997).
CC
-!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 23.1%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 4 VPL 6
Db 1 LPL 3

RESULT 12
FUSS_FUSSO STANDARD; PRT; 8 AA.
ID FUSS_FUSSO
AC P8101;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Allergen Fus s 13596* (Fragment).
OS Fusarium solani (subsp. Pisii) (Neotrichia haematoeccca)
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Neotrichaceae; Neotrichia.
NCBI_TaxID=70791;
RN
RP
SEQUENCE.
RC STRAIN=1ARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RL Submitted (JUN-1997) to Swiss-Prote.
CC
-!- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON_TER 8 8 MW; C372C441F5B69041 CRC64;
SQ SEQUENCE 8 AA; 898 MW;

Query Match 23.1%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3 SVP 5
Db 6 NVP 8

RESULT 13
UPA1_HUMAN STANDARD; PRT; 8 AA.
ID UPA1_HUMAN
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).

OS	Homo sapiens (Human).	AC	P80159;
OC	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DT	01-FEB-1995 (Rel. 31, Created)
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DT	01-FEB-1995 (Rel. 31, Last sequence update)
OX	[1]	DT	16-OCT-2001 (Rel. 40, Last annotation update)
RN		DE	Flagellar filament outer layer protein flaA2 (35 kDa sheath protein)
SEQUENCE		DE	(Fragment).
TISSUE=Plasma		GN	flaA2.
RC		OS	Treponema hydysenteriae (<i>Serpulina hydysenteriae</i>).
RX		OC	Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
RX	Medline:93092937; PubMed:1459097;	NCBI_TaxID=159;	
RA	Hughes G.J.; Frutiger S.; Paquet N.; Ravier F.; Pasquali C., Sanchez J.-C.; James R.; Tissot J.-D.; Bjellqvist B., Hochstrasser D.F.;	[1]	
RT	"Plasma protein map: an update by microsequencing."	RP	SEQUENCE.
RL	Electrophoresis 13:707-714(1992)	STRAIN=CS;	
CC	-1- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown protein is: 4.9, its MW is: 65 kDa.	RX	Medline:93139764; PubMed:1487733;
DR	SWISS-PROTAGE; P30087; HUMAN.	RA	Koopman M.B.H., Baats E., van Vorstebosch C.J.A.H.V., van der Zeijst B.A.M., Kusters J.G.;
FT	NON_TER 1 1	RT	"The periplasmic flagella of <i>Serpulina (Treponema) hydysenteriae</i> are composed of two sheath proteins and three core proteins."
FT	UNSURE 8 8	RT	
FT	NON_TER 8 8	RL	J. Gen. Microbiol. 138:2697-2706(1992).
SQ	SEQUENCE 8 AA; 944 MW;	CC	-1- FUNCTION: Component of the outer layer of the flagella.
Query Match	Score 12; DB 1; Length 8;	CC	-1- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO SHEATH PROTEINS, FLA1 (44 kDa) AND FLA2 (35 kDa) AROUND A CORE THAT CONTAINS THREE PROTEINS FLA1 (37 kDa), FLA2 (34 kDa) AND FLA3 (32 kDa).
Best Local Similarity	23.1%; Pred. No. 1.e+05;	CC	-1- SUBCELLULAR LOCATION: Periplasmic flagellum.
Matches	66.7%; Mismatches 1; Indels 0; Gaps 0;	KW	Flagellum; Periplasmic.
Qy	3 SVP 5 Db 5 NVP 7	FT	FT UNSURE 2 2
RESULT 14		FT	FT NON_TER 8 9
FARS_PENMO	STANDARD; PRT; 9 AA.	SQ	SQ SEQUENCE 9 AA; 1129 MW;
ID	FARS_PENMO		855A19C68B4772D1 CRC64;
AC	P83320;	Query Match	Score 12; DB 1; Length 9;
DT	28-FEB-2003 (Rel. 41, Created)	Best Local Similarity	23.1%;
DT	28-FEB-2003 (Rel. 41, Last sequence update)	Matches	66.7%;
DE	DT 28-FEB-2003 (Rel. 41, Last annotation update)	2;	Mismatches 0;
OS	FMRFamide-like neuropeptide FLPS (SMPSLRLRF-amide).	Indels	0;
Penaeus monodon (Penaeoidea).	RL	Score 12; DB 1; Length 9;	
OC	Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;	Qy	3 SVP 5
Eumalacostraca; Bivalvia; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;	CC	:	
OC	Penaeidae; Penaeus.	Db	2 TVP 4
RN	[1]		
RP	SEQUENCE, AND MASS SPECTROMETRY.		
RC	TISSUE=Eyestalk;		
RX	Medline:21956277; PubMed:111959015;		
RA	Sithigongul P.; Puphem J.; Krungkasem C.; Longyant S., Chaivisuthangkura P.; Sithigongkul W.; Petson A.;		
RA	"Seven novel FMRFamide-like neuropeptide sequences from the eyestalk of the giant tiger prawn <i>Penaeus japonicus</i> ."		
RT	Comp. Biochem. Physiol. 131B:325-337(2002).		
RT	-!- SUBCELLULAR LOCATION: Secreted.		
CC	-!- MASS SPECTROMETRY: MW-1121.1; METHOD-MALDI.		
CC	-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide family).		
CC	GO: GO:0002118; P:neuropeptide signaling pathway; TAS.		
DR	Neuropeptide; Amidation.		
KW	MOD RES 9 9		
FT	AMIDATION.		
SQ	SEQUENCE 9 AA; 1106 MW;		
Query Match	Score 12; DB 1; Length 9;		
Best Local Similarity	23.1%; Pred. No. 1.e+05;		
Matches	66.7%; Mismatches 1; Indels 0; Gaps 0;		
Qy	3 SVP 5		
Db	1 SMP 3		
RESULT 15			
FLA2_TREHY			
ID	FLA2_TREHY		
SEQUENCE	STANDARD;		
PRT;	9 AA.		

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OM protein - protein search, using SW model

Run on: September 5, 2004, 10:59:47 ; Search time 31.6667 Seconds
(Without alignments)
89.674 Million cell updates/sec

Title: US-09-761-636A-14
Perfect score: 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Sequence: 1 C1SVPLVPC 9

Searched: 1017041 seqs., 31518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 10%

Listing first 45 summaries
SPTREMBL_25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rabbit:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:
18: sp_archeap:
19: sp_archeap:
20: sp_archeap:
21: sp_archeap:
22: sp_archeap:
23: sp_archeap:
24: sp_archeap:
25: sp_archeap:
26: sp_archeap:
27: sp_archeap:
28: sp_archeap:
29: sp_archeap:
30: sp_archeap:
31: sp_archeap:
32: sp_archeap:
33: sp_archeap:
34: sp_archeap:
35: sp_archeap:
36: sp_archeap:
37: sp_archeap:
38: sp_archeap:
39: sp_archeap:
40: sp_archeap:
41: sp_archeap:
42: sp_archeap:
43: sp_archeap:
44: sp_archeap:
45: sp_archeap:

Database : SPTREMBL_25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rabbit:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:
18: sp_archeap:
19: sp_archeap:
20: sp_archeap:
21: sp_archeap:
22: sp_archeap:
23: sp_archeap:
24: sp_archeap:
25: sp_archeap:
26: sp_archeap:
27: sp_archeap:
28: sp_archeap:
29: sp_archeap:
30: sp_archeap:
31: sp_archeap:
32: sp_archeap:
33: sp_archeap:
34: sp_archeap:
35: sp_archeap:
36: sp_archeap:
37: sp_archeap:
38: sp_archeap:
39: sp_archeap:
40: sp_archeap:
41: sp_archeap:
42: sp_archeap:
43: sp_archeap:
44: sp_archeap:
45: sp_archeap:

SUMMARIES

ALIGNMENTS

RESULT 1

Q9P8E5
ID Q9P8E5; PRELIMINARY;
AC Q9P8E5; PRT; 9 AA.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HIS4 protein (Fragment).
GN HIS4.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Kluyveromycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OC NCBI_TAXID=28985;
RN [1] RN SEQUENCE FROM N.A.
RN STRAIN=NRR1-Y1140;
RC MEDLINE=99c48382; PubMed=10518937;
RX Lamas-Maceiras M., Esperanza Cerdan E., Freire-Picos M.A.;
RA "Kluyveromyces lactis HIS4 transcriptional regulation: similarities
RT and differences to Saccharomyces cerevisiae HIS4 gene.";
RL FEBS Lett. 458:72-76(1999).
DR AJ238494; CABD125.1; -.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	38.5	9	3 Q9P8E5	Q9P8E5 kluyveromyces
2	19	36.5	7	13 Q42564	Q42564 fugu rubrip
3	19	36.5	8	2 Q56140	Q56140 streptococcus
4	18	34.6	9	13 Q8AYL5	Q8AYL5 carassius a
5	18	34.6	9	13 Q8AUM7	Q8AUM7 carassius a
6	17	32.7	9	10 Q7x6A3	Q7x6A3 zea mays su
7	16	30.8	7	10 Q92333	Q92333 lycopersico
8	16	30.8	8	6 Q02831	Q02831 oryctolagus
9	16	30.8	8	6 Q9TRY3	Q9TRY3 sus sp. ins
10	16	30.8	9	4 Q16220	Q16220 homo sapien
11	16	30.8	9	4 Q9UNF3	Q9UNF3 homo sapien
12	16	30.8	9	12 Q8GVD3	Q8GVD3 ovine respi
13	15	28.8	7	15 Q07624	Q07624 rous sarcoma
14	15	28.8	9	7 Q78225	Q78225 mus musculus
15	15	28.8	9	10 Q9S8J8	Q9S8J8 oryza sativa
16	15	28.8	9	11 Q35953	Q35953 mus musculus

RESULT 2
042564
ID Q42564; PRELIMINARY; PRT; 7 AA.
AC 042564;
DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)	DE	Cytochrome P450 aromatase (Fragment).
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)	GN	CYP19A.
DE	Truncated voltage-gated sodium channel alpha subunit	(Fragment)	OS	<i>Carassius auratus</i> (Goldfish).
SCNBA			OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		OC	Actinopterygii; Neopterygii; Teleostei; Carassius.
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		NCBI_TaxID=7957;	
OC	Tetraodontoidae; Tetraodontidae; Takifugu.		[1]	
OX	NCBI_TaxID=31033;			
RN	SEQUENCE FROM N.A.			SEQUENCE FROM N.A., Kishida M., Wood E., Callard G.V.;
RX	MEDLINE=91442476; PubMed=9295353;			RP Tchoudakova A.V.
RA	Plummer N.W., McBurney M.W., Meisler M.H.;	"Promoter characteristics of two CYP19 genes differentially expressed	RA	in the brain and ovary of teleost fish."
RT	"Alternative splicing of the sodium channel SCN8A predicts a truncated		RT	J. Steroid Biochem. Mol. Biol. 0-0-0(2001).
RT	two-domain protein in fetal brain and non-neuronal cells.";		RL	DR EMBL; AF324897; AN32618.1; -.
RL	J. Biol. Chem. 272:24009-24015(1997).		FT	NON_TER 9
DR	EMBL; U97673; AAB80916.1; -.		FT	SEQUENCE 9 AA; 1060 MW; C49E76D7272B04D CRC64;
GO	GO:0005216; F:ion channel activity; IEA.		SQ	Query Match 34.6%; Score 18; DB 13; Length 9;
KW	Ionic channel.			Best Local Similarity 75.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;
FT	NON_TER 1		QY	6 LVPC 9
SQ	SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;		Db	6 LQPC 9
Query Match 36.5%; Score 19; DB 13; Length 7;				
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
RESULT 3		RESULT 5		
QY	4 VPLV 7	QBADM7 PRELIMINARY; PRT; 9 AA.	QBADM7 ID QBADM7 PRELIMINARY; PRT; 9 AA.	
Db	1 VPLV 4		AC QBADM7; 01-MAR-2003 (TREMBLrel. 23, Created)	
Q56140	PRELIMINARY;	PRT; 8 AA.	DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
AC	Q56140;		DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DT	01-NOV-1996	(TREMBLrel. 01, Created)	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE	STP6 protein (Fragment).		DE CYTOCHROME P450 aromatase (Fragment).	
GN	STP6.		GN CYP19A.	
OS	Streptococcus thermophilus.		OS <i>Carassius auratus</i> (Goldfish).	
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
OC	Streptococcus.		OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
NCBI_TaxID=1308;			OC Cyprinidae; Carassius.	
RN	[1]		NCBI_TaxID=7957;	
RP	SEQUENCE FROM N.A.		RN [1]	
RC	STRAIN=ST11;		RP SEQUENCE FROM N.A., Kishida M., Wood E., Callard G.V.;	
SCRAINE=ST11;			RA Tchoudakova A.V.	
MEDLINE=95047254;			RA "Promoter characteristics of two CYP19 genes differentially expressed	
RX	PubMed=7958782;		RT in the brain and ovary of teleost fish."	
RT	"Isolation and characterisation of promoter regions from Streptococcus		RT J. Steroid Biochem. Mol. Biol. 0-0-0(2001).	
thermophilus".			RL DR EMBL; AF324895; AN32616.1; -.	
RT	FEMS Microbiol. Lett. 122:85-90(1994).		DR EMBL; AF324896; AN32617.1; -.	
DR	EMBL; X78210; CAA55045.1; -.		FT NON_TER 9	
FT	NON_TER 8		FT SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;	
SQ	SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;		QY 6 LVPC 9	
Query Match 36.5%; Score 19; DB 2; Length 8;			Db 6 LQPC 9	
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
RESULT 4		RESULT 6		
QY	2 ISVP 5	Q7X6A3 PRELIMINARY; PRT; 9 AA.	Q7X6A3 ID Q7X6A3 PRELIMINARY; PRT; 9 AA.	
Db	3 ISVP 6		AC Q7X6A3; 01-OCT-2003 (TREMBLrel. 25, Created)	
Q8AYL5	PRELIMINARY;	PRT; 9 AA.	DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)	
AC	Q8AYL5;		DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DT	01-MAR-2003	(TREMBLrel. 23, Created)	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last sequence update)	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
Zea	mays subsp. mays (maize).		DE Isoamylase (Fragment).	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			GN SUI.	
OC			OS Zea mays subsp. mays (maize).	
OC			OC Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae;	
OC			OC Spermatophyta; Andropogoneae; Andropogonidae; Panicoideae;	
PACCAD clade.			OC PACCAD clade; Panicoideae; Andropogoneae; Zea.	

OX	NCBI_TAXID=4578;			OX	NCBI_TAXID=9986;		
RP	[1]			RN	[1]		
SEQUENCE FROM N.A.				SEQUENCE FROM N.A.			
STRAIN=cv. 38-11, and cv. A632;				RX	REPLACEMENT; PubMed=8783186;		
RC	Whitt S.R., Ibanez A.M., Goodman M.M.,			RA	MEDLINE=96377339; PubMed=8783186;		
RA	Buckler E.S. IV;			RA	Metsoanta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,		
RA	"Dissection of maize starch production by candidate gene association,"			RA	Vuorio E.; Evidence for insufficient chondrocytic differentiation during repair of full-thickness defects of articular cartilage.";		
RT	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			RT	Matrix Biol. 15:39-47(1996).		
RL	EMBL: AY290305; APB4531.1; -.			RL	EMBL: S83371; AAC14433.1; -.		
DR	EMBL: AY290311; APB4537.1; -.			KW	Collagen.		
NON_TER	9			FT	NON_TER	1	
SQ	SEQUENCE 9 AA; 976 MW; DF9BCEA76736C6DD CRC64;			SEQUENCE	8 AA; 1028 MW; B859C7272EA77371 CRC64;		
Query Match	32.7%; Score 17; DB 10; Length 9;			Query Match	30.9%; Score 16; DB 6; Length 8;		
Best Local Similarity	66.7%; Pred. No. 1e+06;			Best Local Similarity	100.0%; Pred. No. 1e+06;		
Matches	2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			Matches	2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	7 VPC 9			Qy	8 PC 9		
Db	5 LPC 7			Db	3 PC 4		
RESULT 7				RESULT 9			
P93233				P9TRY3			
ID	P93233			ID	Q9TRY3		
AC	P93233;			AC	Q9TRY3;		
F93233;				PRELIMINARY;			
DT	01-MAY-1997 (TREMBLrel. 03, Created)			DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)			DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	1-aminoacyclopropane-1-carboxylate synthase (EC 4.4.1.14)			DE	Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).		
DE	(Fragment).			OS	Sus sp.		
GN	LE-ACSLB.			OC	Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;		
OS	Lycopersicon esculentum ("Tomato").			OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Subs.		
OC	OC			RA	Shimasaki S., Gao L., Shimonaka M., Ling N.; Isolation and molecular cloning of insulin-like growth factor-binding protein-6.;		
OC	Bukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; asterids; Lamiales; Solanales; Solanaceae; Solanum.			RA	Protein. 5:918-948(1991).		
NCBI_TAXID=4081;				RL	Non-Ter 1 1		
RN				FT	NON_TER 1 1		
RP	SEQUENCE FROM N.A.			FT	NON_TER 1 1		
RX	MEDLINE=97351561; PubMed=9207843;			FT	NON_TER 1 1		
RA	Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;			FT	NON_TER 1 1		
RT	"Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato (Lycopersicon esculentum)."; Plant Mol. 34:275-286(1997).			FT	NON_TER 1 1		
RT	EMBL: U75692; AAC49682.1; -.			FT	NON_TER 1 1		
DR	GO: GO:0016647; F:1-aminocyclopropane-1-carboxylate synthase . . . IBA.			FT	NON_TER 1 1		
DR	GO: GO:0016629; F:Lyase activity; IBA.			FT	NON_TER 1 1		
KW	Lyase.			FT	NON_TER 1 1		
FT	NON_TER 1 1			FT	NON_TER 1 1		
SQ	SEQUENCE 7 AA; 828 MW; 71B412C737741D0 CRC64;			FT	NON_TER 1 1		
Query Match	30.8%; Score 16; DB 10; Length 7;			FT	NON_TER 1 1		
Best Local Similarity	80.0%; Pred. No. 1e+06;			FT	NON_TER 1 1		
Matches	4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			FT	NON_TER 1 1		
Qy	3 SYBLV 7			FT	NON_TER 1 1		
Db	1 SRPLV 5			FT	NON_TER 1 1		
RESULT 8				FT	NON_TER 1 1		
Q02831				FT	NON_TER 1 1		
ID	Q02831;			FT	NON_TER 1 1		
AC	Q02831;			FT	NON_TER 1 1		
DT	01-JUL-1997 (TREMBLrel. 04, Created)			FT	NON_TER 1 1		
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)			FT	NON_TER 1 1		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			FT	NON_TER 1 1		
DE	Pro alpha 1 type III collagen protein (Fragment).			FT	NON_TER 1 1		
OS	Oryctolagus cuniculus (Rabbit).			FT	NON_TER 1 1		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.			FT	NON_TER 1 1		
OC	Nagalila S.R., Spindel E.R.;			FT	NON_TER 1 1		
RT	"Functional analysis of the human gastrin-			FT	NON_TER 1 1		

RT	releasing peptide gene in small cell lung carcinoma cell lines.";	FT	NON_TER	9	9	
RL	Cancer Res. 54:4461-4467(1994).	SQ	SEQUENCE	9	AA;	1154 MW; 8B63EA764541415 CRC64;
DR	EMBL; S73265; AAND4116.; -.					
DR	GO; GO:0005634; C:nucleus; NAS.	Query	Match	30.8%	Score 16;	DB 12; Length 9;
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.	Best Local Similarity	100.0%;	Pred. No. 1e+06;	Mismatches 0;	Indels 0; Gaps 0;
FT	NON_TER	Matches	2;	Conservative	0;	
SQ	SEQUENCE 9 AA;	QY	8 PC 9			
	1070 MW;	Db	6 PC 7			
	77FE37672B040864 CRC64;					
Query Match	30.8%;	Score 16;	DB 4;	Length 9;		
Best Local Similarity	75.0%;	Pred. No. 1e+06;	1;	Mismatches 0;	Indels 0;	Gaps 0;
Matches 3;	Conservative	1;				
SEQUENCE 9 AA;	1067 MW;					
QY	4 VPLV 7	RESULT 13				
Db	:	Q07624	PRELIMINARY;			
	6 LPLV 9	ID	Q07624			
		AC	Q07624;			
		DT	01-NOV-1996 (TREMBLrel. 01; Created)			
		DT	01-NOV-1996 (TREMBLrel. 01; Last sequence update)			
		DT	01-MAR-2003 (TREMBLrel. 23; Last annotation update)			
		DE	WORL.			
		OS	Rous sarcoma virus (strain Prague C).			
		OC	Viruses; Retroviridae; Alpharetroviridae.			
		NCBI_TaxID	11888;			
		RN	[1] _			
		RP	SEQUENCE FROM N.A.			
		RX	MEDLINE=93010967; PubMed=1327749;			
		RA	Donze O.; Spair P. F.;			
		RA	"Role of the open reading frames of Rous sarcoma virus leader RNA in			
		RT	translational and genome packaging";			
		RL	EMBO J. 11:3147-3175(1992).			
		DR	EMBL; X67587; CAA428661; -.			
		SQ	SEQUENCE 7 AA; 672 MW;	776045A76B7DD6F0 CRC64;		
Query Match	28.8%;	Score 15;	DB 15;	Length 7;		
Best Local Similarity	50.0%;	Pred. No. 1e+06;	1;	Mismatches 1;	Indels 0;	Gaps 0;
Matches	2;	Conservative	1;			
QY	5 PLVP 8	RESULT 14				
Db		Q78225	PRELIMINARY;			
	4 PSIP 7	ID	Q78225			
		AC	Q78225;			
		DT	01-NOV-1998 (TREMBLrel. 08; Created)			
		DT	01-NOV-1998 (TREMBLrel. 08; Last sequence update)			
		DT	01-DEC-2001 (TREMBLrel. 19; Last annotation update)			
		DB	Lymphocyte antigen (Fragment).			
		OS	Mus musculus (Mouse).			
		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
		OC	Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.			
		NCBI_TaxID	10090;			
		RN	[1] _			
		RP	SEQUENCE FROM N.A.			
		RC	STRAIN=CRO435; TISSUE=Kidney;			
		RX	MEDLINE=88084418; PubMed=33692165;			
		RA	Golubic M.; Budimir O.; Schoepfer R.; Kasahara M.; Mayer W.E.,			
		RA	Figueroa F.; Klein J.;			
		RT	"Nucleotide sequence analysis of class II genes borne by mouse t			
		OS	chromosomes.";			
		RL	Genet. Res. 50:137-146(1987).			
		DR	EMBL; L38589; AAA57293.1; -.			
		FT	NON_TER	1		
		FT	NON_TER	1		
		SQ	SEQUENCE 9 AA; 1143 MW;	9E681772C729C33A CRC64;		
Query Match	28.8%;	Score 15;	DB 7;	Length 9;		
Best Local Similarity	100.0%;	Pred. No. 1e+06;	0;	Mismatches 0;	Indels 0;	Gaps 0;
Matches	3;	Conservative	0;			
QY	2 ISVPLVP 8	RESULT 15				
Db		Q78225	PRELIMINARY;			
	1 MQIPOQAP 7	ID	Q78225			
		AC	Q78225;			
		DT	01-JUN-2002 (TREMBLrel. 21; Created)			
		DT	01-JUN-2002 (TREMBLrel. 21; Last sequence update)			
		DE	Matrix Protein 2 (Fragment).			
		GN	M2.			
		OS	Ovine respiratory syncytial virus.			
		OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;			
		CC	Paramyxoviridae; Pneumovirinae; Pneumovirus.			
		OX	[1] _			
		RN	SEQUENCE FROM N.A.			
		NCBI_TaxID	28865;			
		RX	Medline=21580655; PubMed=11724134;			
		RA	Elerlay N.Z.; Kania S.A.; Potgieter L.N.;			
		RA	"The ovine respiratory syncytial virus F gene sequence and its			
		RT	diagnostic application.";			
		RL	J. Vet. Diagn. Invest. 13:455-461(2001).			
		DR	EMBL; AF334398; AAL91343.1; -.			

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Db      ||| 5 LVP 7
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RESULT 15
Q9S8J8          PRELIMINARY;      PRT;      9 AA.
ID   Q9S8J8
AC   Q9S8J8;
DT   01-MAY-2000 (TREMBrel. 13, Created)
DT   01-MAY-2000 (TREMBrel. 13, Last sequence update)
DT   01-OCT-2002 (TREMBrel. 22, Last annotation update)
DE   ORYZATENSIN=IOACTIVE peptide.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoidae; Oryzeae; Oryza.
NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95102521; PubMed=7804141;
RA   Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R. ;
RT   "Isolation and characterization of oryzatensin: a novel bioactive
RT   peptide with ileum-contracting and immunomodulating activities derived
RT   from rice albumin." ;
RL   Biochem. Mol. Biol. Int. 33:1151-1158(1994).
DR   Gramene; Q9S8J8; -1093 MW; 0EBC67377B56877B CRC64;
SEQUENCE 9 AA;
```

Query Match Score 15; DB 10; Length 9;

Best Local Similarity 28.8%; Prod. No. 1e-06;
Matches 50.0%; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVP 8

DB 3 PMYP 6

Search completed: September 5, 2004, 11:05:43
Job time : 32.6667 secs

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Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	9	4 AAU04533	Aau04533 VEGF base
2	27	51.9	9	5 ABG35134	Abg35134 Pancreati
3	27	51.9	9	5 ABG46931	Abb46931 Desmocoil
4	27	51.9	9	6 ABG60522	Abg60522 Selective
5	27	51.9	9	6 ABG56920	Abg56920 Pancreati
6	26	50.0	7	3 AAY784998	Aay784998 Amino aci
7	26	50.0	7	7 ADC44293	Adc44293 Endotheli
8	26	50.0	9	3 AAY63242	Aay63242 Protocad
9	26	50.0	9	4 AAE07204	Aae07204 Modified
10	26	50.0	9	4 AAM24655	Aam24655 Human MHC
11	26	50.0	9	5 ABG35050	Abg35050 Endostati
12	25	48.1	5	2 AAY95843	Aay95843 IGF-1 mut
13	25	48.1	5	3 AAY784999	Aay784999 Amino aci
14	25	48.1	5	7 ADC44308	Adc44308 Endotheli
15	24	46.2	6	2 AAY03909	Aay03909 Hepatitis
16	24	46.2	9	1 AAP10098	Aap10098 Sequence
17	24	46.2	9	4 ABP21743	Abp21743 HIV A03 m
18	24	46.2	9	5 AAU94456	Aau94456 Human nov
19	24	46.2	9	5 AAU94653	Aau94653 Human nov
20	24	46.2	9	7 ADC44488	Adc44488 Endotheli
21	24	46.2	9	7 ADC59359	Adc59359 GST bindi
22	23	44.2	6	2 AAW85926	Aaw85926 Rodent IL
23	23	44.2	6	6 ABP9702	Abp9702 Human sec
24	23	44.2	7	4 AAB64710	Aab64710 Human sec
25	23	44.2	7	4 AAU04530	Aau04530 VEGF base

peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is cardiovascular, retinopathy, psoriasis, arthropathy, haemangioma, vasculitis, malignant or benign tumour, post recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, vasculature. The peptides are used to image blood vessels and lymphatic vessels. The nonomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

Sequence 9 AA;

Query Match	100.0%	Score 52;	DB 4;	Length 9;
Best Local Similarity	100.0%	Pred. No. 1.4e+06;	Mismatches 0;	Indels 0;
Gaps	0;			

XX

Sequence 9 AA;

Query Match	100.0%	Score 52;	DB 4;	Length 9;
Best Local Similarity	99.9%	Pred. No. 1.4e+06;	Mismatches 0;	Indels 0;
Gaps	0;			

XX

RESULT 2
ABG35134 standard; peptide; 9 AA.

AC ABG35134;
DT 15-JUL-2002 (first entry)
DE Pancreatic islet targeting peptide #10.
OS Targeting peptide; cancer; Hodgkin's disease; cytostatic; immunosuppressive; anti-inflammatory; antibacterial; diabetes mellitus; antiatherosclerotic; antidiabetic; anticancer; autoimmune disease; bacterial infection; viral infection.
XX Unidentified.
PN WO200202722-A2.
XX 08-SEP-2000; 2000US-0231266P.
PD 14-MAR-2002.
PA (TEXA) UNIV TEXAS SYSTEM.
XX Arap W, Pasqualini R;

XX DR WPI; 2002-383050/41.

XX Identifying targeting peptides useful for treating e.g. diabetes mellitus, inflammatory diseases, cancer, or autoimmune diseases, comprises exposing a sample to a phage display library and recovering phage bound to the sample.

XX Claim 56; Page 288; 298pp; English.
PS

XX This invention relates to a novel method for identifying disease CC targeting peptides. The method comprises exposing a sample from an organ CC tissue or cell type of interest, to a phage display library and CC recovering phage bound to the sample (the phage expresses targeting CC peptides). The peptides identified by the method of the invention may CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic, CC antiatherosclerotic, antidiabetic, antibacterial and antiviral CC activities. The methods and composition are useful for identifying CC targeting peptides and one or more receptors for a targeting peptide. The CC targeting peptides are used for selective delivery of therapeutic agents, CC including gene therapy vectors and fusion proteins, to specific organs, CC tissues, or cell types in subject. The targeting peptide may also be used CC for treating diseases such as diabetes mellitus, inflammatory diseases, CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and CC viral infections and Hodgkin's disease. The present sequence represents a CC targeting peptide of the invention
XX Sequence 9 AA;

Query Match 1 CISYPLVPC 9
Best Local Similarity 51.9%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0;
Gaps 0;
SQ

Query	1 CISYPLVPC 9	Score 27;	DB 5;	Length 9;
Best Local Similarity	55.6%;	Pred. No. 1.4e+06;	Mismatches 3;	Indels 0;
Matches	5;	Conservative 1;	Mismatches 3;	Indels 0;
Gaps	0;			

RESULT 3

ABB46931
ID ABB46931 standard; peptide; 9 AA.
XX AC ABB46931;
XX DT 30-JAN-2002 (first entry)
DB Desmocollin-2 CAR cyclic peptide 13.
XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytosatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
XX OS Synthetic.
XX WO200172956-A2.

XX PR 27-MAR-2000; 2000US-00335852.
XX PD 04-OCT-2001.
XX PF 27-MAR-2001; 2001WO-IB001400.
XX PP 27-MAR-2000; 2000US-00335852.
XX PA (ADHEREX TECHNOLOGIES INC.
XX PI Blaschuk OW, Symonds JM, Gour BJ;
XX DR WPI; 2002-025778/03.
XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin
PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
XX PS Claim 23; Page 111; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal Cadherin CAR CC sequence, a substance such as an antibody or antigen-binding fragment CC that specifically binds a desmosomal cadherin CAR sequence and/or a CC polynucleotide encoding a polypeptide that comprises a desmosomal CC cadherin CAR sequence or analogue. The modulating agents have

CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer (e.g.
 CC carcinoma, leukaemia or melanoma) and induce apoptosis
 XX Sequence 9 AA;

Qy	1 CISVPLVPC 9	Score 27; DB 5; Length 9;
Best Local Similarity	44.4%;	Pred. No. 1.4e+05;
Matches	4;	Mismatches 4;
Db	1 CTAFATPPC 9	Indels 0; Gaps 0;

RESULT 4
 ABG60522 ID ABG60522 standard; peptide; 9 AA.

XX AC AC AFATPPC 9

RESULT 5
 ABRS56920 ID ABRS56920 standard; peptide; 9 AA.

XX AC AC AFATPPC 9

Query Match 51.9%; Score 27; DB 5; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1.4e+06;
 Matches 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CISVPLVPC 9

Db 1 CMSSPGVAC 9

RESULT 5
 ABRS56920 ID ABRS56920 standard; peptide; 9 AA.

XX AC AC AFATPPC 9

XX DE Pancratic targeting peptide SEQ ID NO:137.

XX DT 30-JUL-2003 (First entry)

XX KW Targeting peptide; obesity; lipodystrophy; anorectic; antilipaemic;
 KW peptide therapy; gene therapy; infection; human immunodeficiency virus;
 KW HIV; Placental delivery; teratogenic; placenta; adipose; pancreatic;
 KW beta-3 integrin; beta-5 integrin; spleen; amineopeptidase A.

XX DE OS Mus musculus.

XX OS Synthetic.

XX PN WO2003022991-A2.

XX PD 20-MAR-2003.

XX PF 30-AUG-2002; 2002WO-US027836.

XX PR 07-SEP-2001; 2001WO-US027692.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Pasqualini R, Arap W, Kolonin MG;

XX XX DR WPI; 2003-371749/35.

XX PT Treating obesity or a lipodystrophy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to a subject.

XX PT XX Example 9; Page 114; 247pp; English.

XX PS XX The present invention describes a method for treating obesity or a lipodystrophy, which comprises: (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; (d) inducing weight loss in the subject or treating lipodystrophy. The adipose targeting peptides have anorectic and antilipaemic activities, and can be used in peptide and gene therapy. The method is used for treating obesity or a lipodystrophy that is related to infection with human immunodeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for teratogenic activity. ABRS56920 to ACC79106 to ACC7911 represent sequences used in the exemplification of the present invention

XX Sequence 9 AA;

Qy 1 CISVPLVPC 9

Db 1 CMSSPGVAC 9

Query Match 51.9%; Score 27; DB 6; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1.4e+06;
 Matches 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CISVPLVPC 9

Db 1 CMSSPGVAC 9

Sequence 9 AA;

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin 5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; Lf-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX Synthetic.
 OS Homo sapiens.

XX Key Location/Qualifiers
 PH Disulfide-bond 1. .9

FT WO957149-A2.
 PN 11-NOV-1999.
 PD XX
 PF 05-MAY-1999; 99WO-SA0000363.
 PR 05-MAY-1998; 98US-00073940.
 PR 06-NOV-1998; 98US-00187059.
 PR 20-JAN-1999; 99US-00234195.
 PR 08-MAR-1999; 99US-00264516.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 PI Blaschuk OW, Gour BJ, Byers S;
 XX DR WPI; 2000-038791/03.
 PT New cadherin modulating agents, used for modulating nonclassical cadherin
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX PS Claim 84; Page 201; 252pp; English.
 XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion or nonclassical-cadherin expressing cells in a mammal,
 CC enhancing delivery of a drug through the skin of a mammal,
 CC enhancing adhesion of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vascular permeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age-
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY44643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX Sequence 9 AA;

Query Match 50.0%; Score 26; DB 3; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

SQ Sequence 9 AA;

Query Match 50.0%; Score 26; DB 4; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CISVPLVFC 9
 Db 1 CPALDLVTC 9

Db : :||| 1 CLPLPLPV 7

RESULT 10
 AAM24655 standard; peptide; 9 AA.
 ID AAM24655
 XX
 AC AAM24655;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DB Human MHC class I molecule HLA-A2 binding 83P5G4 peptide #32.
 XX
 KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
 KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
 KW chromosome 1q31-q32.
 XX
 OS Homo sapiens.
 XX
 PN WO200159115-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004426.
 XX
 PR 09-FEB-2000; 2000US-01B1261P.
 XX
 PA (UROG-) UROGENEWS INC.
 PI Hubert RS, Afar DEH, Challita-Eid PM, Paris M, Levin E,
 Mitchell SC, Jakobovits A,
 DR 2001-514669 /56.
 XX
 PT An isolated 83P5G4-related protein useful as a diagnostic and/or
 PT therapeutic agent in multiple cancers such as prostate, bladder and bone
 cancer.
 XX
 PS Example 15; Page 77; 112pp; English.

The polypeptide sequences represent the 83P5G4-related protein and
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
 CC expression in normal adult tissue, but it is also aberrantly expressed in
 many cancers including tumours of the prostate, testis, bladder, kidney,
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
 peptide fragments and specific PCR primers are therefore useful for
 CC diagnosing and treating cancer. A vector comprising a polynucleotide
 CC which encodes a single chain monoclonal antibody, that immunospecifically
 binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
 CC preparation of a composition for treating a patient with a cancer that
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and
 CC tissue and to thereby detect the presence of cancerous cells
 XX
 SQ Sequence 9 AA;

Query Match 50.0%; Score 26; DB 4; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e-06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISVPLVPC 9
 : :||| |
 DB 2 LPLPLRPC 9

RESULT 12
 AAR95843
 ID AAR95843 standard; peptide; 5 AA.
 XX
 AC AAR95843;
 DT 26-JUN-1996 (first entry)
 XX

RESULT 11
 ABG35050 standard; peptide; 9 AA.
 ID ABG35050

DB IGF-1 mutein C67 residues 63-67.
 XX Insulin-like growth factor-1; IGF-1; polyethylene glycol; PEG; triflate;
 KW IGF-1/PEG conjugate; maleimide; sulphhydryl; thiol; tresylate; aziride;
 KW exirane; 5-pyridyl; therapy; dwarfism; diabetes; periodontal disease;
 KW osteoporosis.
 XX OS Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 5 /note= "ASC"
 FT XX
 PT XX
 PR XX
 PN WO9532003-A1.
 XX PA 30-NOV-1995.
 XX PP 24-MAY-1995; 95WO-US006540.
 XX PR 24-MAY-1994; 94US-00248273.
 XX (AMGE-) AMGEN BOULDER INC.
 XX PI Cox GN, McDermott MJ, Ko C;
 XX DR WPI; 1996-020360/02.
 XX PT Conjugates for treatment of, e.g. dwarfism, diabetes, or osteoporosis - comprising polyethylene glycol attached to mutein of IGF at free cysteine.
 XX PT Example 2: Page 22; 48pp; English.
 XX PS Sequence 5 AA;
 XX SQ AAR9532-R5844 represent the altered fragments of the insulin-like growth factor-1 (IGF-1) muteins of the invention. This sequence represents the N-terminal residues 63-67 of the IGF-1 mutein C67. The wild type IGF-1 sequence is represented by AAR87744. These muteins contain a non-native cysteine residue substituted for one of the first (or last) four amino acid residues of this sequence. Polyethylene Glycol (PEG) conjugates are then created from the muteins, where the PEG is attached to the non-native cysteine residue. The PEG is attached to the free cysteine through an activating group selected from maleimide, sulphhydryl, thiol, triflate, tresylate, aziride, exirane or 5-pyridyl. The conjugates can also comprise a second polypeptide attached to the PEG. The conjugates may be used for the treatment of IGF associated conditions, such as dwarfism, diabetes, periodontal disease or osteoporosis. Advantages associated with these conjugates are that they have a higher molecular weight, and an extended circulating half life in comparison to wild type IGF.

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 2;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 1;	
		Indels 0;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches 0;	
		Indels 1;	Gaps 0;

XX SQ Sequence 5 AA;

Query Match	Score 25;	DB 3;	Length 5;
Best Local Similarity	80.0%;	Prod. No. 1.4e+06;	
Matches	4;	Mismatches	

PN WO2003037172-A2.
 XX PR 11-AUG-1997; 97US-0055186P.
 PD XX PA (BOEH) BOHRINGER INGELHEIM CANADA LTD.
 XX XX PI Linas-Brunet M, Poupart M, Rancourt J, Simoneau B, Tsantrizos Y;
 PF XX PI Werner D;
 XX XX WPI; 1999-167361/14.
 PR New peptides inhibitors of NS3 protease - useful for treatment of
 PT hepatitis C infections.
 PA (GPCB) GPC BIOTECH INC.
 XX PS Disclosure; Page 108; 158pp; English.
 XX New generically described Peptides are disclosed which are NS3 protease
 PR inhibitors useful for treating hepatitis C virus (HCV) infection. The
 PT present sequence represents a specific example of these peptides. In a
 CC test to determine inhibition in a NS3 protease/NS4A cofactor peptide
 CC radiometric assay, this peptide had an IC50 value of 92 micromolar
 XX SQ Sequence 6 AA;
 Query Match 46.2%; Score 24; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 Lypc 9
 |||
 Db 3 Lypc 6

XX Novel synthetic or recombinant polypeptide useful for promoting reducing
 PR proliferation and/or migration of endothelial cells, and for modulating
 PT angiogenesis, has endothelial cell binding protein sequences.
 XX Claim 3; SEQ ID NO 36; 126pp; English.
 PS
 XX The invention relates to a novel isolated, synthetic or recombinant
 CC peptide or polypeptide which includes one or more endothelial cell
 CC binding protein (ECBP) sequences. A peptide of the invention has anti-
 CC tumour, cytostatic, vasoconstrictive, antipsoriatic, dermatological,
 CC ophthalmological, antidiabetic, antiarthritic, vulnerary, antiulcer,
 CC antiinflammatory, antibacterial, and gynaecological activity. The peptide
 CC is useful for promoting, reducing, the proliferation and/or migration of
 CC endothelial cells, by treating the cells with an ECBP agonist, which is
 CC preferably the peptide, to promote proliferation and/or migration of the
 CC treated cells, and for reducing or promoting angiogenesis, by treating
 CC the cells with ECBP antagonist, which is preferably the peptide of the
 CC invention. A peptide of the invention is also useful for manufacturing a
 CC medicament for promoting angiogenesis, by admixing an ECBP agonist or
 CC ECBP antagonist to promote or reduce angiogenesis at one or more sites in
 CC a treated mammal. The medicament is useful for promoting or reducing
 CC angiogenesis. ECBP sequences are useful to alter the infectivity spectrum
 CC of a viral particle. The present sequence represents an ECBP of the
 CC invention.
 XX SQ Sequence 5 AA;
 Query Match 48.1%; Score 25; DB 7; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 VPLVP 8
 :|||
 Db 1 IPLYP 5

XX RESULT 15
 ID AAY03909 standard; peptide; 6 AA.
 XX AAY03909;
 AC
 DT 08-JUN-1999 (first entry)
 DE Hepatitis C inhibitor peptide.
 XX KW Hepatitis C; inhibitor; NS3 protease; NS4A cofactor.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-Ac-Asp"
 XX PN WO9907733-A2.
 XX PD 18-FEB-1999.
 XX PP 10-AUG-1998; 98WO-CA000765.

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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:05:54 ; Search time 35.667 Seconds
 79.502 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVPLVPC 9

Scoring table: BLOSUM22

Gapext 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 119143

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%
 Maximum Match 100%

Database : Published Applications Aa:
 1: /cgn2_6_ptodata/2/pubpaas/US07_PUBCOMB.pep:
 2: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US06_NEW_PUB.pep:
 3: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US07_PUBCOMB.pep:
 4: /cgn2_6_ptodata/2/pubpaas/US06_PUBCOMB.pep:
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 6: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US08_PUBCOMB.pep:
 7: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US08_NEW_PUB.pep:
 8: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US09_PUBCOMB.pep:
 9: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US09A_PUBCOMB.pep:
 10: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US09B_PUBCOMB.pep:
 11: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US09C_PUBCOMB.pep:
 12: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US09_NEW_PUB.pep:
 13: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US10A_PUBCOMB.pep:
 14: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US10B_PUBCOMB.pep:
 15: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US10C_PUBCOMB.pep:
 16: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US10_NEW_PUB.pep:
 17: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US60_NEW_PUB.pep:
 18: /cgn2_6_ptodata/2/pubpaas/2/pubpaas/US60_PUBCOMB.pep:
 Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	52	100.0	9	9	US-09-761-636A-14	Sequence 14, Appl
2	27	51.9	9	12	US-10-363-208-242	Sequence 242, App
3	27	51.9	9	15	US-10-154-884B-11221	Sequence 11221, A
4	27	51.9	9	15	US-10-154-884B-11228	Sequence 11228, A
5	27	51.9	9	15	US-10-154-884B-11250	Sequence 11250, A
6	27	51.9	9	15	US-10-154-884B-11254	Sequence 11254, A
7	27	51.9	9	15	US-10-154-884B-11258	Sequence 11258, A
8	27	51.9	9	15	US-10-154-884B-11259	Sequence 11259, A
9	27	51.9	9	15	US-10-154-884B-11265	Sequence 11265, A
10	27	51.9	9	15	US-10-154-884B-11285	Sequence 11285, A
11	27	51.9	9	15	US-10-154-884B-11280	Sequence 11280, A
12	26	50.0	7	14	US-10-386-457-21	Sequence 21, Appl
13	26	50.0	9	9	US-09-780-053-148	Sequence 148, App
14	26	50.0	9	12	US-10-63-208-137	Sequence 137, App
15	26	50.0	9	14	US-10-006-869-2726	Sequence 2726, Ap

RESULT 1
 US-09-761-636A-14
 ; GENERAL INFORMATION:
 ; Patent No. US2002005218A1
 ; PRIORITY APPLICATION NUMBER: US/09761636A
 ; CURRENT FILING DATE: 2001-01-18
 ; PRIORITY FILING DATE: 2000-01-18
 ; FILE REFERENCE: 1064/48505 Achien et al
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 14
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-761-636A-14

Query Match 100.0%; Score 52; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CISVPLVPC 9
 Db 1 CISVPLVPC 9

RESULT 2
 US-10-363-208-242
 ; Sequence 242, Application US/10363208
 ; Publication No. US20040048243A1

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; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 242
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-208-242

RESULT 4
US-10-154-884B-11228
; Sequence 11228, Application US/10154884B
; Publication No. US2004005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Rettter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US 60/200,545
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11230
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11228
Query Match Score 27; DB 12; Length 9;
Best Local Similarity 51.9%; Pred. No. 1.2e+06;
Matches 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CISVPLVPC 9
Db 1 CMSSPFCAAC 9

RESULT 3
US-10-154-884B-11221
; Sequence 11221, Application US/10154884B
; Publication No. US2004005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane A.
; APPLICANT: Rettter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11230
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11221
Query Match Score 27; DB 15; Length 9;
Best Local Similarity 51.9%; Pred. No. 1.2e+06;
Matches 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CISVPL 6
Db 4 CLSVPV 9

RESULT 5
US-10-154-884B-11250
; Sequence 11250, Application US/10154884B
; Publication No. US2004005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Rettter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US

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CURRENT APPLICATION NUMBER: US/10/154, 884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 6/0/186, 126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 6/0/190, 479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 6/0/200, 545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 6/0/200, 303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 6/0/200, 779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 6/0/200, 999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 6/0/202, 084
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 6/0/218, 950
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 11254
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11254

RESULT 6
US-10-154-884B-11254
; Sequence 11254, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algare, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154, 884B
; PRIOR APPLICATION NUMBER: US 6/0/186, 126
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: US 6/0/190, 479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 6/0/200, 545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 6/0/200, 303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 6/0/200, 779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 6/0/200, 999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 6/0/202, 084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 6/0/206, 201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 6/0/218, 950
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11258

RESULT 7
US-10-154-884B-11258
; Sequence 11258, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algare, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154, 884B
; PRIOR APPLICATION NUMBER: US 6/0/186, 126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 6/0/190, 479
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 6/0/200, 545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 6/0/200, 303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 6/0/200, 779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 6/0/200, 999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 6/0/202, 084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 6/0/206, 201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 6/0/218, 950
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11258

Query Match      51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CISVPL 6
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Db      4 CLSVPV 9

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RESULT 8
; Sequence 11259, Application US/10154884B
; Publication No. US2004000561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-01521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 10/154, 884B
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186, 126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190, 479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200, 545
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; PRIOR APPLICATION NUMBER: US 60/200, 303
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; PRIOR APPLICATION NUMBER: US 60/200, 779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200, 999
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; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/202, 084
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; PRIOR FILING DATE: 2000-05-22
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; PRIOR APPLICATION NUMBER: US 60/222, 903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 11265
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-154-884B-11265

Query Match      51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CISYPL 6
     |:|||:
Db   4 CLSYPLV 9

RESULT 10
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; Publication No. US2004000561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 10/154, 884B
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186, 126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190, 479
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200, 545
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200, 303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200, 999
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/202, 084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/205, 201
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/218, 950
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 11275
; LENGTH: 9

Query Match      51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CISYPL 6
     |:|||:
Db   4 CLSYPLV 9

RESULT 9
; Sequence 11265, Application US/10154884B
; Publication No. US2004000561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-01521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 10/154, 884B
; PRIOR FILING DATE: 2000-01-01
; PRIOR APPLICATION NUMBER: US 60/186, 126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190, 479
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 11275
; LENGTH: 9

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; SEQ ID NO 137
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-208-137

Query Match      50.0%; Score 26; DB 12; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy          1 CISYBLVPC 9
          | :| |
Db          1 CRSLLPPVRC 9

RESULT 15
US-10-006-869-2726
; Sequence 2726, Application US/10006669
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 1000086-407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2726
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-10-006-869-2726

Query Match      50.0%; Score 26; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy          1 CISYBLVPC 9
          | :| |
Db          1 CFALDLVTC 9

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Search completed: September 5, 2004, 11:16:00
Job time : 35.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using SW mode.

Run on: September 5, 2004, 11:01:38 ; Search time 12 Seconds
(without alignments)

38.719 Million cell updates/sec

Title: US-09-761-636A-14
Perfect score: 52
Sequence: 1 CISVPLVPC 9

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 89883

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Maximum Match 100%

Listing First 45 summaries

Database :	Issued_Patents_AA:
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2:	/cgmn_6/ptodata/2/iaa/5B_COMB_pep:*
3:	/cgmn_6/ptodata/2/iaa/6A_COMB_pep:*
4:	/cgmn_6/ptodata/2/iaa/6B_COMB_pep:*
5:	/cgmn_6/ptodata/2/iaa/PCTOUS_COMB_pep:*
6:	/cgmn_6/ptodata/2/iaa/backtfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	51.9	9	4 US-09-535-852-1681	Sequence 1681, App
2	26	50.0	9	4 US-09-187-859-2726	Sequence 2726, App
3	24	50.0	9	4 US-09-539-542B-2/26	Sequence 2726, App
4	46.2	7	1	US-08-261-206A-18	Sequence 18, App
5	23	44.2	8	1 US-08-189-331-147	Sequence 147, App
6	23	44.2	8	1 US-08-189-331-148	Sequence 148, App
7	23	44.2	8	1 US-08-189-331-149	Sequence 149, App
8	23	44.2	8	1 US-08-189-331-150	Sequence 150, App
9	23	44.2	8	2 US-08-533-760-9	Sequence 9, App
10	23	44.2	8	2 US-08-471-068-147	Sequence 147, App
11	23	44.2	8	2 US-08-471-068-148	Sequence 148, App
12	23	44.2	8	2 US-08-471-068-149	Sequence 149, App
13	23	44.2	8	2 US-08-471-068-150	Sequence 150, App
14	23	44.2	9	3 US-08-591-2/1-4	Sequence 4, App
15	23	44.2	9	3 US-09-558-754-373	Sequence 373, App
16	23	44.2	9	3 US-09-042-107-373	Sequence 373, App
17	23	44.2	9	4 US-09-937-59-19	Sequence 19, App
18	23	44.2	9	4 US-09-722-250D-373	Sequence 373, App
19	22	42.3	4	3 US-09-357-952-69	Sequence 69, App
20	22	42.3	4	4 US-09-521-651-69	Sequence 69, App
21	22	42.3	4	4 US-09-168-888-69	Sequence 69, App
22	22	42.3	5	3 US-09-357-952-68	Sequence 68, App
23	22	42.3	5	3 US-09-357-952-116	Sequence 116, App
24	22	42.3	5	4 US-09-521-650-68	Sequence 68, App
25	22	42.3	5	4 US-09-521-650-116	Sequence 116, App
26	22	42.3	5	4 US-09-168-888-68	Sequence 68, App
27	22	42.3	5	4 US-09-168-888-116	Sequence 116, App

ALIGNMENTS

RESULT 1 US-09-535-852-1681					
; Sequence 1681, Application US/09535852					
; GENERAL INFORMATION:					
; Patent No. 6658911					
; APPLICANT: Blasciuk, Orest W.					
; SYMONDS, James M.					
; GOUR, Barbara J.					
; TITLE OF INVENTION: DESMOCOLLIN-2 CELL ADHESION RECOGNITION SEQUENCE					
; FILE REFERENCE: 100086 407C6					
; CURRENT APPLICATION NUMBER: US/09/535,852					
; CURRENT FILING DATE: 2001-05-21					
; NUMBER OF SEQ ID NOS: 2009					
; SOFTWARE: FastSEQ for Windows Version 4.0					
; SEQ ID NO: 1681					
; LENGTH: 9					
; TYPE: PRT					
; ORGANISM: Artificial Sequence					
; FEATURE:					
; OTHER INFORMATION: Cyclized modulating agent comprising desmocollin-2 cell adhesion recognition sequence					
US-09-535-852-1681					
Query Match					
Best Local Similarity					
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;					
Qy	1 CISVPLVPC 9				
	[: :				
Db	1 CIAFATTPC 9				

RESULT 2
US-09-187-859-2726

; Sequence 150, Application US/09187859A					
; Patent No. 6358920					
; GENERAL INFORMATION:					
; APPLICANT: Blasciuk, Orest W.					
; GOUR, Barbara J.					
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CADHERIN-MEDIATED FUNCTIONS					
; FILE REFERENCE: 100086 407C1					
; CURRENT APPLICATION NUMBER: US/09/187, 859A					
; CURRENT FILING DATE: 1998-11-06					
; NUMBER OF SEQ ID NOS: 4052					
; SOFTWARE: PatentIn Ver. 2.0					
; SEQ ID NO: 18726					
; LENGTH: 9					
; TYPE: PRT					

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-261-206A-18

; Query Match 50.0%; Score 26; DB 4; Length 9;
; Best Local Similarity 44.4%; Pred. No. 3e+05; Mismatches 2; Indels 0; Gaps 0;
; Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CISVPLVPC 9
Db 1 CFALDLVTC 9

; RESULT 3
; Sequence 2726, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gaur, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086 407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2726
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-839-542B-2726

; Query Match 50.0%; Score 26; DB 4; Length 9;
; Best Local Similarity 44.4%; Pred. No. 3e+05; Mismatches 2; Indels 0; Gaps 0;
; Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CISVPLVPC 9
Db 1 CFALDLVTC 9

; RESULT 5
; Sequence 147, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-730-9090
; TELEFAX: 212-869-3864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Peptide
; US-08-189-331-147

; RESULT 4
; Sequence 18, Application US/08261206A
; Patent No. 554007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; TITLE OF INVENTION: With Thrombin
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

Query Match Similarity 44.2%; Score 23; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 3e+05; 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 1; Indels 0;

RESULT 6
 US-08-189-331-148
 ; Sequence 148, Application US/08189331
 ; GENERAL INFORMATION:
 ; APPLICANT: Kay, B. K.
 ; APPLICANT: Fowlkes, D. M.
 ; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
 ; NUMBER OF SEQUENCES: 186
 ; COMPUTER READABLE FORM:
 ; ADDRESSER: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/189.331
 ; FILING DATE: Concurrently herewith
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 5747334
 ; REFERENCE/DOCKET NUMBER: 1101-155
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9050
 ; TELEFAX: 212 869-8864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 149:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-189-331-149

Query Match Similarity 44.2%; Score 23; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 3e+05; 1; Mismatches 1; Indels 0;
 Matches 3; Conservative 1; Gaps 0;

RESULT 8
 US-08-189-331-150
 ; Sequence 150, Application US/08189331
 ; Patent No. 5747334
 ; GENERAL INFORMATION:
 ; APPLICANT: Kay, B. K.
 ; APPLICANT: Fowlkes, D. M.
 ; TITLE OF INVENTION: totally synthetic affinity reagents
 ; NUMBER OF SEQUENCES: 186
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/189.331
 ; FILING DATE: Concurrently herewith
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 5747334
 ; REFERENCE/DOCKET NUMBER: 1101-155
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9050
 ; TELEFAX: 212 869-8864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 150:

SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: Peptide
 US-08-189-331-150

Query Match 44.2%; Score 23; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 3e+05; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 3; Conservative 1;

QY 1 CISVP 5
 Db 1 CYSAP 5

RESULT 9
 US-08-633-760-9
 ; Sequence 9, Application US/086333760

GENERAL INFORMATION:
 ; Patent No. 5803429
 ; APPLICANT: NIWA, MINEO
 ; APPLICANT: SAITO, YOSHIMASA
 ; APPLICANT: FUJIMURA, TAKAO
 ; APPLICANT: ISHII, YOSHINORI
 ; APPLICANT: NOGUCHI, YUJI
 ; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
 ; ADDRESS: P.C.
 ; STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: USA
 ; ZIP: 22202

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/633,760
 FILING DATE: 01-MAY-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 18-929-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEX: 248855 OPAT UR

SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-633-760-9

Query Match 44.2%; Score 23; DB 1; Length 8;
 Best Local Similarity 42.9%; Pred. No. 3e+05; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 3; Conservative 3;

QY 1 CISPIV 7
 Db 2 CAAVPLM 8

RESULT 10

RESULT 11
 US-08-471-068-148
 ; Sequence 148, Application US/08471068

GENERAL INFORMATION:
 ; Patent No. 5948335
 ; APPLICANT: KAY, B. K.
 ; APPLICANT: Fowles, D. M.
 ; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
 ; NUMBER OF SEQUENCES: 186
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/08/471,068
 APPLICATION NUMBER: US/08/471,068
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/189,331
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-155
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 148:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-471-068-148
 Query Match 44.2%; Score 23; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 3e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CISVP 5
 Db 3 CVSAP 7

RESULT 13
 US-08-471-068-150
 Sequence 150, Application US/08471068
 ; Patent No. 5948635
 ; GENERAL INFORMATION:
 ; APPLICANT: Kay, B. K.
 ; ATTORNEY: Fowlkes, D. M.
 ; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
 ; NUMBER OF SEQUENCES: 186
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 115 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/471,068
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/189,331
 ; TELECOMMUNICATION INFORMATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; TELEPHONE: 212 790-9050
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 150:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-471-068-150

Query Match 44.2%; Score 23; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 3e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CISVP 5
 Db 1 CVSAP 5

RESULT 14
 US-08-891-271-4
 Sequence 4, Application US/08891271
 ; Patent No. 6165476

GENERAL INFORMATION:
 i APPLICANT: Strom, Terry B.
 i APPLICANT: Sytkowski, Arthur J.
 i APPLICANT: Zheng, Xin Xiao
 i TITLE OF INVENTION: Fusion Proteins with an Immunoglobulin
 i TITLE OF INVENTION: Hing Region Linker
 i NUMBER OF SEQUENCES: 35
 i CORRESPONDENCE ADDRESS:
 i ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
 i STREET: Two Militia Drive
 i CITY: Lexington
 i STATE: Massachusetts
 i COUNTRY: USA
 i ZIP: 02173
 i COMPUTER READABLE FORM:
 i MEDIUM TYPE: Floppy disk/
 i COMPUTER: IBM PC compatible
 i OPERATING SYSTEM: PC-DOS/MS-DOS
 i SOFTWARE: PatentIn Release #1.0, Version #1.30
 i CURRENT APPLICATION DATA:
 i APPLICATION NUMBER: US/08/891,271
 i FILING DATE: 10-JUL-1997
 i CLASSIFICATION: 435
 i ATTORNEY/AGENT INFORMATION:
 i NAME: Hogle, Doreen M.
 i REGISTRATION NUMBER: 36,361
 i REFERENCE/DOCKET NUMBER: RIH97-07
 i TELECOMMUNICATION INFORMATION:
 i TELEPHONE: 617-861-6240
 i TELEFAX: 617-861-9540
 i INFORMATION FOR SEQ ID NO: 4:
 i SEQUENCE CHARACTERISTICS:
 i LENGTH: 9 amino acids
 i TYPE: amino acid
 i STRANDEDNESS: single
 i TOPOLOGY: linear
 i MOLECULE TYPE: peptide
 i US-08-891-271-4

Query Match 44.2%; Score 23; DB 3; Length 9;
 Best Local Similarity 80.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

Qy 5 PLVPC 9
 Db 4 PLVAC 8

RESULT 15
 US-09-258-754-373
 i Sequence 373, Application US/09258754
 i Patent No. 6174687
 i GENERAL INFORMATION:
 i APPLICANT: Ruoslahti, Erkki
 i APPLICANT: Pasqualini, Renata
 i APPLICANT: Rajotte, Daniel
 i TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
 i Title of Invention: Membrane Dipeptidase
 i FILE REFERENCE: P-LJ 3443
 i CURRENT APPLICATION NUMBER: US/09/258,754
 i CURRENT FILING DATE: 1999-02-26
 i EARLIER APPLICATION NUMBER: 09/042,107
 i EARLIER FILING DATE: 1998-03-13
 i NUMBER OF SEQ ID NOS: 452
 i SOFTWARE: PatentIn Ver. 2.0
 i SEQ ID NO: 373
 i LENGTH: 9
 i TYPE: PRT
 i ORGANISM: Artificial Sequence
 i FEATURE:
 i OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 i US-09-258-754-373

total number of hits satisfying chosen parameters:
searched: 283366 seqs, 96191526 residues

minimum DB seq length: 0
maximum DB seq length: 2000000000
RESULT 1
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (Fragment)

post-processing: Minimum Match 0%
Maximum Match 100%
C:Species: Rana pipiens (northern leopard frog)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C:Accession: A39035

R; Ardelt, W.; Mikalski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
Amino acid sequence of an anti-tumor protein from Dana ruminans occur-

A; Reference number: A39035; MUID:91093131; PMID:1985896
A; Accession: A39035

D-22 No. 1066 number 25
J: P14242; *
A; status: preliminary
A; molecule type: protein
A; residues: 1-104 <ARD>

FIGURE NO. 1. Line number or results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Best local Similarity 61.5%; Pred. No. 1.7;
 Matches 8; Conservative 1; Mismatches 4;
 Indels 0; Gaps 0;

	Score	Query	Match	Length	DB	ID	Description
result No.							
1	CASELIGKSNTTFC	13	Qy	1	-----		

1	43	59.7	104	2 A39035
2	41	56.9	397	2 AC1574
3	41	56.9	397	2 AM1220
				ribonuclease-relat acerate kinase hom nuclease kinase hom

				kinase homolog Ack2 [imported] - <i>Listeria innocua</i> (strain Clip11262)
				KBSL2
				AC174
4	40	55.6	383	2
			T17722	
4	39	54.2	409	6
			S42384	
5	54	54.1	119	6
			S42385	
6	54	54.1	119	6
			S42386	

```
#text_change 14-Dec-2001
C.Species: Listeria innocua
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
C.Accession: AC1574
```

9	37	51.4	319	2	A84947	LYT-B protein [impo	R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.
10	37	51.4	421	2	S53818	XPM2 protein - Af	; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.
11	37	51.4	433	2	S70914	Pectinesterase (EC	D.; Jones, L.M.; Karst, U.

protein kinase C (Science 294, 849-852, 2001).
 Authors: Kieft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madiueno, N.; Maitouroff, A.; Vazquez-Boland, J.A.; Voss, W.
 Ok, C.; Schlueter, T.; Simoes, N.; Triarrez, A.

A;Title: Comparative genomics of *Listeria* species. A;Reference number: AB1077; MUID:2153279; PMID:11679669

A;Cross-references: GB:AL592022; PIDN:CAC96363.1; PID:g16413591; GSDB:GN00177
A;Experimental source: strain Cip11262
A;Residues: 1-397 <GLA>
probable RNA helicase (EC 3.1.11.
catalase (EC 1.11.
C30A5.5 protein -

C;Genetics: ACKA2
C;Superfamily: acetate kinase

Query	Match	Score	41%	DB	Length
germin homolog F21		56.9%			397
Best Local Similarity		72.7%			
Best Local Match			No. 14;		
Max. Score			No. 14;		
Min. Score			No. 14;		
Avg. Score			No. 14;		
SD			No. 14;		

QY	1 CASELGKSTNT 11	submitted to the EMBL Data Library, March 1994
Db	214 CAIEGKSYNT 224	A;Reference number: S42368 A;Accession: S42364 A;Status: preliminary A;Molecule type: DNA A;Cross-references: EMBL:Z300662; NID:9459581; PID:9459587
RESULT 3		AH1220 acetate kinase homolog AckA2 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Accession: AH1220 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsthi, H.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A;Authors: Kraft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:2153729; PMID:11679669 A;Accession: AH1220 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-397 <GLA> A;Cross-references: GB:NC_003210; PIDN:CAC99246_1; PID:916410584; GSPDB:GN00177 A;Experimental source: strain EGD-e C;Genetics: A;Gene: AckA2 C;Superfamily: acetate kinase
QY	1 CASELGKSTNT 11	Query Match 56.9%; Score 41; DB 2; Length 397; Best Local Similarity 72.7%; Pred. No. 14; Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db	214 CAIEGKSYNT 224	A;Reference number: Z18806 A;Accession: T17722 A;Status: preliminary; translated from GB/EMBL/DBJ A;Molecule type: DNA A;Residues: 1-383 <GRA> A;Cross-references: EMBL:U42580; NID:94028896; PIDN: AAC96599_1 A;Experimental source: specific host Chlorella strain NC64A C;Genetics: A;Note: A231L
RESULT 4		T17722 hypothetical protein A231L - Chlorella virus PBCV-1 C;Species: Chlorella virus PBCV-1 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T17722 R;Graves, M.V.; Van Etten, J.L. submitted to the EMBL Data Library, May 1999 A;Reference number: Z18806 A;Accession: T17722 A;Status: preliminary; translated from GB/EMBL/DBJ A;Molecule type: DNA A;Residues: 1-383 <GRA> A;Cross-references: EMBL:U42580; NID:94028896; PIDN: AAC96599_1 A;Experimental source: specific host Chlorella strain NC64A C;Genetics: A;Note: A231L
QY	1 CASELGKSTNTFC 13	Query Match 55.6%; Score 40; DB 2; Length 383; Best Local Similarity 46.2%; Pred. No. 21; Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Db	304 CVMNGKRNNEFC 316	A;Reference number: A96500; MUID:21353325; PMID:21353325 A;Accession: G97177 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-378 <KUR> A;Cross-references: GB:AE001437; PIDN:AAK80210_1; PID:915025255; GSPDB:GN00168 A;Experimental source: Clostridium acetylbutylicum ATCC824 C;Genetics: A;Gene: CAC2253
RESULT 5		S42384 Kruppel-like protein - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Sep-1997 C;Accession: S42384 R;Smith, A.
QY	1 CASELGKSTNT 11	Query Match 52.8%; Score 38; DB 2; Length 378; Best Local Similarity 66.6%; Pred. No. 47; Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

378 CASDTEKSTTT 398

LA SOUTERRAIN 388

A. S. GOLDBECK AND J. R. HARRIS

RESULTS 8

Q46AC2-like protein - Arabidopsis thaliana
;Alternate names: protein T9C5;120
;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

Q46AC2 submitted to the Protein Sequence Database, December 1999
Reference number: Z23026
Accession: T46230

RESULTS 9

SELGKSTNTF 12
| :||| | |||
260 SELGSSYNTF 269

SELGKSTNTF 12
| :||| | |||
260 SELGSSYNTF 269

SELGKSTNTF 12
| :||| | |||
232 AELKGKETGTF 241

RESULTS 10

PM02 protein - African clawed frog
;Species: Xenopus laevis (African clawed frog)
;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000

PM02 submitted to the EMBL Data Library, February 1996
Reference number: S53818; PMID:9515750; MUID:553818

RESULTS 11

S70914 pectinesterase (EC 3.1.1.11) precursor - Erwinia chrysanthemi
N: Alternate names: pectin methylesterase
C: Species: Erwinia Chrysanthemi
C: Accession: S70914; S70913
R: Shevchik, V.E.; Condemine, G.; Hugouvieux-Cotte-Pattat, N.; Robert-Baudouy, J. submitted to the EMBL Data Library, February 1995
A: Description: Characterization of pectin methylesterase B, an outer membrane protein
A: Reference number: S70914
A: Accession: S70914
A: Molecular type: DNA
A: Residues: 1-433 <SHE>
A: Cross-references: EMBL:X84665; PIDN:CAA591511.1; PID:91212890; R: Shevchik, V.E.; Condemine, G.; Hugouvieux-Cotte-Pattat, N.; Robert-Baudouy, J.
Mol. Microbiol. 19, 455-466, 1996
A: Title: Characterization of pectin methylesterase B, an outer membrane lipoprotein
A: Reference number: S70913; MUID:962228695; PMID:8830237
A: Accession: S70913
A: Status: nucleic acid sequence not shown
A: Molecular type: DNA
A: Residues: 1-53-124-161 <SHA>
A: Cross-references: EMBL:X84665; PIDN:CAA591511.1
A: Experimental source: strain 3937
C: Genetics:
A: Gene: pemB
A: Start codon: GTG
C: Superfamily: Pectinesterase_PemB
C: Keywords: carboxylic ester hydrolase
P: 1-21-Domain: signal sequence #status predicted <SIG>
P: 22-433/Product: pectinesterase #status predicted <MAT>

Query Match 51.4%; Score 37; DB 2; Length 433;
Best Local Similarity 46.2%; Pred. No. 81;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Query Match 51.4%; Score 37; DB 2; Length 433;
Best Local Similarity 46.2%; Pred. No. 81;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULTS 12

S35362 protein kinase C (EC 2.7.1.-) pck1 - fission yeast (Schizosaccharomyces pombe)
N: Alternate names: pombe C-kinase 1
C: Species: Schizosaccharomyces pombe
C: Accession: S35362; R37866; T33203
R: Toda, T.; Shimanuki, M.; Yanagida, M. EMBO J. 12, 1987-1995, 1993
A: Title: Two novel protein kinase C-related genes of fission yeast are essential
A: Reference number: S55362; MUID:93229141; PMID:8491190
A: Accession: S35362
A: Molecular type: DNA
A: Residues: 1-988 <TOD>
A: Cross-references: EMBL:D14337; PIDN:BAA03267.1; PID:9303938; R: Churcher, C.M.; Barrett, B.G.; Andreadis, M.A.; Walsh, S.V. submitted to the EMBL Data Library, February 1996

A;Reference number: 221750
A;Accession: T37866
A;Molecule type: DNA
A;Residues: 93-988 <DEV>
A;Cross-references: EMBL:Z69795; PIDN:CAA93697.1; GSPDB:GN00066; SPDB:SPAC17G8.14C
R;Grishchuk, K.; McIntosh, J.R.; Devlin, K.; Churcher, C.; Barrell, B.G.; Rajandream, M.
Submitted to the EMBL Data Library, February 1996
A;Reference number: 221778
A;Accession: T38203
A;Molecule type: DNA
A;Residues: 1-16, 'AMVASTKNP', 36-137 <GR>
A;Cross-references: EMBL:Z69730; PIDN:CAA93602.1; GSPDB:GN00066; SPDB:SPAC22H10.01C
A;Experimental source: strain 972h-; cosmid c22H10
C;Genetics:
A;Gene: Pck1
A;Map position: 1L
A;Introns: 767/2; 834/3; 897/3; 959/1
C;Superfamily: yeast protein kinase C; protein kinase C zinc-binding repeat homology; protein kinase C ATP duplication; phospholipid binding; phosphotransferase; serine/threonine kinase; zinc-binding repeat homology <K21>
F;481-530/Domain: protein kinase C zinc-binding repeat homology <K21>
F;662-923/Domain: protein kinase C zinc-binding repeat homology <KIN>
F;670-678/Region: protein kinase ATP-binding motif

Query Match Score 51.4%; DB 1; Length 98;
Best Local Similarity 66.7%; Pred. No. 1.B+02/
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 5 LGKSTNTFC 1.3
Db 8.17 LGNTTSFC 825

RESULT 13
T43051
protein kinase C (EC 2.7.1.-) PKC1 - fungus *Cochliobolus heterostrophus*
C;Species: *Cochliobolus heterostrophus*, Bipolaris maydis
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43051
A;Status: preliminary; translated from GB/EMBL/DDBJ
R;Oester, B.M.
FEMS Microbiol. Lett. 165, 273-280, 1998
A;Title: PKC1, encoding a protein kinase C, and FAT1, encoding a fatty acid transporter
A;Reference number: Z223033; MUID:38415124; PMID:3742699
A;Accession: T43051
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1174 <QES>
A;Cross-references: EMBL:Y15839; NID:92687848; PIDN:CAA75801.1; PID:92687849
C;Genetics:
A;Gene: pck1
A;Introns: 146/1; 234/1; 559/1; 952/2; 1019/3; 1155/1
C;Superfamily: yeast protein kinase C; protein kinase C zinc-binding repeat homology; protein kinase C ATP; phospholipid binding; phosphotransferase; serine/threonine-specific protein kinase; zinc-binding repeat homology <K21>
F;527-576/Domain: protein kinase C zinc-binding repeat homology <K2N2>

Query Match Score 51.4%; DB 2; Length 1294;
Best Local Similarity 58.3%; Pred. No. 2.3e+02/
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CASELGKSTNTFC 12
Db 1161 CGERLGIMNTFC 1172

RESULT 15
S09778
hypothetical protein UL16 precursor - human cytomegalovirus (strain AD169)
C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: S09778
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Hornshell, T.; M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A;Reference number: S09749; MUID:90269039; PMID:2161319
A;Accession: S09778
A;Molecule type: DNA
A;Residues: 1-230 <CHB>
A;Cross-references: EMBL:X117403; NID:959591; PIDN:CAA3548.1; PMID:959520
A;Note: this sequence was submitted to the EMBL Data Library, December 1989
C;Superfamily: human cytomegalovirus hypothetical protein UL16
C;Keywords: glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-230/Product: hypothetical protein UL16 #status predicted <NAT>
F;189-206/Domain: transmembrane #status predicted <TMN>

RESULT 14
S77690
probable membrane protein YOL075C - yeast (*Saccharomyces cerevisiae*)
A;Alternative names: hypothetical protein Oli125; hypothetical protein Oli130; hypothetical protein Oli131
C;Species: *Saccharomyces cerevisiae*
C;Accession: S77690; S66767; S66768
A;Reference number: S77690
A;Accession: S77690
A;Molecule type: DNA
A;Residues: 1-230 <CHB>

RESULT 15
S09778
hypothetical protein UL16 precursor - human cytomegalovirus (strain AD169)
C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: S09778
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Hornshell, T.; M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A;Reference number: S09749; MUID:90269039; PMID:2161319
A;Accession: S09778
A;Molecule type: DNA
A;Residues: 1-230 <CHB>
A;Cross-references: EMBL:X117403; NID:959591; PIDN:CAA3548.1; PMID:959520
A;Note: this sequence was submitted to the EMBL Data Library, December 1989
C;Superfamily: human cytomegalovirus hypothetical protein UL16
C;Keywords: glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-230/Product: hypothetical protein UL16 #status predicted <NAT>
F;189-206/Domain: transmembrane #status predicted <TMN>

Sun Sep 5 10:36:29 2004

us-09-761-636a-5.open.rpr

Page 5

F,35,41,68,84,95,101,132,145/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 50.7%; Score 36.5; DB 2; Length 230;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
Qy 1 CASENG-KSTNTFC 13
| : | | | : | | : |
Db 25 CNDLGSKSSNSTC 38

Search completed: September 5, 2004, 10:01:14
Job time : 11.9798 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.						
protein - protein search, using sw model						
Search time 5.90909 Seconds (without alignments) 114.554 Million cell updates/sec						
September 5, 2004, 09:38:39 ; Search time 5.90909 Seconds (without alignments) 114.554 Million cell updates/sec						
title:	US-09-761-636A-5					
refct score:	72					
sequence:	1 CASELGKSTNTFC 13					
scoring table:	BLOSUM62					
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searched:	141681 seqs, 52070155 residues					
total number of hits satisfying chosen parameters: 141681						
DB seq length:	0					
maximum DB seq length:	2000000000					
post-processing:	Minimum Match 0%					
	Maximum Match 100%					
	Listing first 45 summaries					
database:	SwissProt 42.2					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
result No.	Score	Query	Match	Length	DB	ID
1	54	75.0	354	1	VEGD_HUMAN	Q43915 homo sapiens
2	51	70.8	326	1	VEGD_RAT	P35211 ratius norvegicus
3	51	70.8	358	1	VEGD_MOUSE	P97946 mus musculus
4	43	59.7	104	1	RN30_BANPI	P22069 rana pipiens
5	41	56.9	397	1	ACK2_LISMO	P92399 listeria monocytogenes
6	41	56.9	397	1	ACK2_LISMO	Q8Y7v1 listeria monocytogenes
7	39	54.2	451	1	YNV5_GAEEL	P34568 caenorhabditis elegans
8	37	51.4	169	1	IIF9_HUMAN	Q9nzN8 homo sapiens
9	37	51.4	319	1	ISP9_BUCAI	P57247 buchnera aculeata
10	37	51.4	407	1	RPE2_HUMAN	O60858 homo sapiens
11	37	51.4	433	1	PMEB2_BRWCH	P047474 erwinia chrysanthemi
12	37	51.4	988	1	PKC1L_SCHPO	P36582 schizosaccharomyces pombe
13	37	51.4	1174	1	KPC1_COCHE	O42632 cochliobolus heterostrophus
14	37	51.4	1294	1	YOH57_BEAST	Q02834 saccharomyces cerevisiae
15	36.5	50.7	230	1	UL16_HCMVA	P16759 human cytomegalovirus
16	36	50.0	282	1	PPNK_HALN1	Q9hnX7 halobacter
17	36	50.0	282	1	YK86_GAEEL	P33569 streptomyces coelicolor
18	36	50.0	483	1	BCA_STRVL	P57781 micropropogaea
19	36	50.0	673	1	ESR2_MICUN	O14081 schizosaccharomyces pombe
20	36	50.0	944	1	TPSK_XENLA	Q9Ptd7 xenopus laevis
21	36	50.0	1360	1	ISP1_HUMAN	P75439 mycoplasma genitalium
22	35.5	49.3	224	1	Y243_NYCPN	P67715 human sapiens
23	35.5	49.3	2156	1	PR1_HUMAN	P08900 centruroides
24	35	48.6	66	1	SCX2_CENSU	O13547 saccharomyces cerevisiae
25	35	48.6	238	1	CW14_FEAST	Q8K9z4 buchnera aculeata
26	35	48.6	313	1	ISP1_BUCAI	Q9kuy6 vibrio cholerae
27	35	48.6	61	1	ALR1_VIBCH	P47599 mycoplasma pneumoniae
28	35	48.6	393	1	ACKA_NYCGE	Q9pp18 campylobacter jejuni
29	35	48.6	396	1	ACKA_CAMJE	Q89aqo1 buchnera aculeata
30	35	48.6	576	1	FTS1_BUCBP	P24082 escherichia coli
31	35	48.6	602	1	TRAN_ECOLI	P59749 thiazobium
32	35	48.6	855	1	FNU1_EHIA2	P03379 human immunodeficiency virus type 1
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	35	48.6	1517	1	GUTB_ECOLI	P09831 escherichia
	37	48.6	1941	1	KUJLA_ECOLI	O60014 kluveromy
	38	48.6	7389	1	BPA1_MOUSE	O11926 mus musculu
	39	48.6	7389	1	IF6_YEAST	Q11522 saccharomy
	40	47.9	245	1	SP18_YEAST	P32572 saccharomy
	41	47.9	300	1	PERP_BACSU	O31605 bacillus su
	42	47.9	609	1	RNR_EUCAL	P57528 buchnera ap
	43	47.9	731	1	UTP_PIG	Q29100 sus scrofa
	44	47.2	122	1	CRT1_XENLA	Q91174 xenopus lae
	45	47.2	335	1		

ALIGNMENTS

scoring table: BLOSUM62

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searched: 141681 seen 520701 55 received

total number of hits satisfies chosen parameters.

total number of hits satisfies chosen parameters.

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Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0%	
	Maximum Match 100%	
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DT	10-OCT-2003 (Rel. 42, Last annotation update)	
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DE	FIGF OR VEGFD.	
GN	Homo sapiens (Human).	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomii; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OC	NCBI_TaxID=9606;	
OC	[1]	
RN		
RP	SEQUENCE FROM N.A.	

SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	%
1	54	75.0	354	1	VEGD_HUMAN	043915 homo sapiens
2	51	70.8	326	1	VEGD_RAT	035251 rattus norvegicus
3	51	70.8	358	1	VEGD_MOUSE	P97946 mus musculus
4	43	59.7	104	1	RN30_RANPI	P22069 rana pipiens
5	41	56.9	397	1	ACK2_LISMO	Q92cm9 listeria monocytogenes
6	41	56.9	397	1	ACK2_LISMO	Q8Y7v1 listeria monocytogenes
7	39	54.2	451	1	YNV5_CAEEL	P34568 caenorhabditis elegans
8	31	51.4	169	1	LIIF9_HUMAN	Q9nzh8 homo sapiens
9	37	51.4	1	1SPH_BUCAI	P57279 buchnera aculeata	
10	37	51.4	407	1	RPF2_HUMAN	060858 homo sapiens
11	37	51.4	433	1	PMEB_BRWCH	Q47474 erwinia chrysanthemi
12	37	51.4	988	1	PCKL_SCHPO	P36582 schizosaccharomyces pombe
13	37	51.4	1174	1	KPC1_COCHE	042632 cochliobolus heterostrophus
14	37	51.4	1294	1	YOH5_YEAST	Q08234 saccharomyces cerevisiae
15	36.5	50.7	230	1	UL16_HCMVA	P16759 human cytomegalovirus
16	36	50.0	282	1	PPNK_HALN1	Q9hnx7 halobacterium
17	36	50.0	282	1	YK86_GABEL	P34352 caenorhabditis elegans
18	36	50.0	483	1	BKA_STRVL	P33569 streptomyces thermophilus
19	36	50.0	673	1	ESR2_MICUN	P57781 micropogonaceae
20	36	50.0	944	1	TPSK_SCHPO	O14081 schizosaccharomyces pombe
21	36	50.0	1360	1	CING_XENPLA	Q9Ptd7 xenopus laevis
22	35.5	49.3	224	1	Y24_3_MYCPN	P75439 mycoplasma pneumoniae
23	35.5	49.3	2156	1	RP1_HUMAN	P56715 homo sapiens
24	35	48.6	66	1	SCX2_CENSUS	P08900 centruroides sculpturatus
25	35	48.6	238	1	CW14_YEAST	Q13547 saccharomyces cerevisiae
26	35	48.6	313	1	ISP8_BUCAP	QBk9z4 buchnera aculeata
27	35	48.6	361	1	ALR1_VIBCH	Q9kuy5 vibrio cholerae
28	35	48.6	393	1	ACKA_MYCGE	P47599 mycoplasma genitalium
29	35	48.6	396	1	ACKA_CAMPE	Q9Ppl8 campylobacter pylori
30	35	48.6	576	1	FTSI_BUCPB	Q89aq7 buchnera aculeata
31	35	48.6	602	1	TRAN_ECOLI	P24082 escherichia coli
32	35	48.6	758	1	PARC_RHIME2	Q57949 rhizobium leguminosarum
33	35	48.6	855	1	ENVN_HVIA2	P03379 rhizobium immutans

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Krzywinski M.I., Skalska U., Smilus D.E., Butterfield Y.S.N., Krywinski M.I., Skalska U., Smilus D.E., Schnarch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL [5] RP PROCESSING AND SEQUENCE OF 89-94; 100-105 AND 206-213.

RX MEDLINE=20011413; PubMed=10542248;

RA Stacker S.A., Stevers K.L., Caesar C., Moritz R.J., Karpanen T., Nice E.C., Roufail S., Simpson R.J., Moritz R., Karpanen T., Alitalo K., Achen M.G.;

RA "Biogenesis of vascular endothelial growth factor-D involves proteolytic processing which generates non-covalent homodimers.,";

RT J. Biol. Chem. 274:32127-32136(1999).

RL -; FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.

CC -; SUBUNIT: Homodimer; non-covalent and antiparallel.

CC -; TISSUE SPECIFICITY: Highly expressed in lung, heart, small intestine and fetal lung, and at lower levels in skeletal muscle, colon, and pancreas.

CC -; PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions.

CC -; SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

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CC EMBL; D89630; BAA24264.1; -.

DR EMBL; Y12863; CAA73370.1; -.

DR EMBL; Y12864; CAA73371.1; -.

DR EMBL; Y12865; CAA73371.1; JOINED.

DR EMBL; Y12866; CAA73371.1; JOINED.

DR EMBL; Y12867; CAA73371.1; JOINED.

DR EMBL; Y12868; CAA73371.1; JOINED.

DR EMBL; Y12869; CAA73371.1; JOINED.

DR EMBL; Y12870; CAA73371.1; JOINED.

DR EMBL; AJ000185; CAA00942.1; -.

DR EMBL; BC027948; AAH22948.1; -.

DR HSSP; P15632; 1VPP.

DR Genew; HGNC:3708; FIGER.

DR MIM; 300091; -.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0005161; P:platelets-derived growth factor receptor bin. . . ; TAS.

DR GO; GO:0005102; F:receptor binding; TAS.

DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.

DR InterPro; IPR001153; CX3C repeat.

DR InterPro; IPR00072; PD_growth_factor.

DR Pfam; PF03128; CX3C; 3.

DR Pfam; PF00341; PDGF; 1.

DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS00249; PDGF_1.

DR PROSITE; PS00278; PDGF_2.

KW Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.

CC 1 SIGNAL 21 POTENTIAL.

FT PROPEP 22 OR 99 (IN A MINOR FORM).

FT CHAIN 89 VASCULAR ENDOTHELIAL GROWTH FACTOR D.

FT PROPEP 205

FT DOMAIN 222 354 4 X 16 AA REPEATS OF C-X (10) -C-X-C-

FT REPEAT 222 318 X(1,3)-C.

FT REPEAT 227 1 (APPROXIMATE).

FT REPEAT 258 237 1.

FT REPEAT 277 293 2.

FT REPEAT 301 318 3.

FT DISULFID 111 153 BY SIMILARITY.

FT DISULFID 142 189 BY SIMILARITY.

FT DISULFID 146 191 BY SIMILARITY.

FT DISULFID 136 136 INTERCHAIN (BY SIMILARITY).

FT CARBOHYD 145 145 INTERCHAIN (BY SIMILARITY).

FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 354 AA; 40444 MW; 20480769D735173E CRC64;

Query Match 75.0% Score 54; DB 1; Length 354;

Best Local Similarity 100.0%; Pred. No. 0.018; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 2 ASPLGKSTNTF 12

Db 121 ASPLGKSTNTF 131

RESULT 2

ID VEGD_RAT STANDARD; PRT; 326 AA.

ID VEGD_RAT STANDARD; PRT; 326 AA.

AC 03251; DT 28-FEB-2003 (Rel. 41, Created)

AC 03251; DT 28-FEB-2003 (Rel. 41, Last sequence update)

AC 03251; DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Vascular endothelial growth factor D precursor (VEGF-D) (c-Fos induced growth factor) (FIGF).

GN FIGF OR VEGFD.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Murinae; Rattus.

OC NCBI_TaxID=10116; RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Sprague-Dawley; RA Yamada Y., Hirata Y., Nezu J., Shimane M.;

RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

CC -; FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-3 (Flt4) receptor (By similarity).

CC -; SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).

CC -; SUBCELLULAR LOCATION: Secreted (By similarity).

CC -; PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity).

CC -; SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

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CC -; CC DR AF014827; AAB66557.1; -.

REPEAT 282 298 3.
 FT 306 323 4.
 FT DISULFID 116 158 BY SIMILARITY.
 FT DISULFID 147 194 BY SIMILARITY.
 FT DISULFID 151 196 BY SIMILARITY.
 FT DISULFID 141 141 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 150 150 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ 358 AA; 40908 MW; 6638B17PBF07037 CRC64;

Query Match 70.8%; Score 51; DB 1; Length 358;
 Best Local Similarity 90.3%; Pred. No. 0.066;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASELGKSTNTF 12
 Db 126 ASELGKTTNTF 136

RESULT 4
 RN30_RANPI STANDARD; PRT; 104 AA.
 ID RN30_RANPI
 AC P22659;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 OS Rana pipiens [EC 3.1.27.] (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
 OX NCBI_TaxID=8404;
 RN [1] _
 RP SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=91093131; PubMed=11985896;
 RA Ardelte W.; Mikulski S.M.; Shogen K.;
 RT "Amino acid sequence of an anti-tumor protein from Rana pipiens
 oocytes and early embryos. Homology to pancreatic ribonuclease.";
 RL J. Biol. Chem. 266:245-251(1991).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=93066156; PubMed=1438177;
 RA Mosmann S.C., Johns K.L., Ardelte W., Mikulski S.M., Shogen K.,
 James M.N.G.;
 RT "Comparative molecular modeling and crystallization of P-30 protein:
 a novel antitumor protein of Rana pipiens oocytes and early
 embryos.";
 RL Proteins 14:392-400(1992).
 RN [3]
 RX X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
 RX MEDLINE=94165079; PubMed=8120892;
 RA Mosmann S.C., Ardelte W., James M.N.G.;
 RT "A X-ray crystallographic structure of P-30 protein, an
 amphibian ribonuclease with anti-tumor activity.";
 RL J. Mol. Biol. 236:1141-1153 (1994).
 CC -|- SIMILARITY: Basic protein with antiproliferative/cytotoxic activity
 against several tumor cell lines in vitro as well as antitumor
 in vivo. It exhibits ribonuclease-like activity against high
 molecular weight ribosomal RNA.
 CC -|- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
 CC -|- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR PDB:1ONC; 31-JAN-94.
 DR InterPro:IPR001427; RNaseA.
 DR Pfam:PF00074; rnaseA; 1.
 DR SMART:SN00092; RNASE_P; 1.
 DR PROSITE:PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolase; Nucleic acidlease; Endonuclease; 3D-structure;
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 1 1
 ACT-SITE 10 10

FT ACT SITE 31 31
 FT ACT SITE 97 97
 FT DISULFID 19 68
 FT DISULFID 30 75
 FT DISULFID 48 90
 FT DISULFID 87 104
 FT HELIX 3 10
 FT STRAND 11 12
 FT HELIX 19 22
 FT TURN 23 24
 FT STRAND 26 30
 FT STRAND 33 38
 FT HELIX 41 45
 FT HELIX 46 48
 FT TURN 49 50
 FT STRAND 55 58
 FT TURN 63 70
 FT STRAND 74 75
 FT STRAND 77 84
 FT TURN 86 91
 FT STRAND 92 93
 FT STRAND 94 101
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 59.7%; Score 43; DB 1; Length 104;
 Best Local Similarity 61.5%; Pred. No. 0.57; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
 Db 75 CKYLUKKSTNKFC 87

RESULT 5
 ACK2_LISIN STANDARD; PRT; 397 AA.
 ID ACK2_LISIN
 AC Q92C9N; (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acetate kinase 2 (EC 2.7.2.1) (Acetokinase 2).
 GN ACK2 OR LIN1132.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=16162;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / Serovar 6a;
 RX MEDLINE=21532779; PubMed=11679669;
 RA Charbit A., Chetouani F., Couve E., de Darvvar A., Brandt P., Chakraborty T.,
 RA Baquero F., Berche P., Bloecker H., Durand L., Dussurget O.,
 RA Glaser P., Frangeul L., Buchrieser C., Rustin C., Russiok C., Amend A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Enrion K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.M., Kretz J., Kuhn M., Kunst F., Kurppkat G.,
 RA Madueno E., Maftouram A., Mata Vicente J., NG E., Nedjari H.,
 RA Nordsielk G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remell B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 RL Science 294:849-852 (2001).
 CC -|- CATALYTIC ACTIVITY: ATP + acetate = ADP + acetyl phosphate.
 CC -|- PATHWAY: Conversion of acetyl-CoA to acetyl phosphate; first step.
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -|- SIMILARITY: Belongs to the acetokinase family.

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CC or send an email to license@isb-sib.ch).

CC	EMBL; AL996167; CAC96367..1;	DR	Pfam; PF00871; Acetate kinase; 1.
CC	PIR; AC1574; AC1574..-	DR	PRINTS; PR00411; ACETATEKINASE.
DR	ListiList; LIN01132..-	DR	TIGRFAMS; TIGR00016; ackA; 1.
DR	HAMAP; MF 00020; ..1.	DR	PROSITE; PS01075; ACETATE_KINASE_1; 1.
DR	InterPro; IPR000890; Acetate_kin.	DR	PROSITE; PS01076; ACETATE_KINASE_2; 1.
DR	InterPro; IPR00437; AckA.	KW	Transferase; Kinase; Complete_Kinase.
DR	Pfam; PF00871; Acetate kinase; 1.	SEQUENCE	397 AA; 43132 MW; 6E295AE9A5PDS5CB CRC64;
DR	PRINTS; PR00471; ACETATEKINASE.	Query Match	56.9%; Score 41; DB 1; Length 397;
DR	TIGRFAMS; TIGR00016; ackA; 1.	Best Local Similarity	72.7%; Pred. No. 5.2;
DR	PROSITE; PS01075; ACETATE_KINASE_1; 1.	Matches	8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
DR	PROSITE; PS01076; ACETATE_KINASE_2; 1.	Qy	1 CASELGKSTNT 11
SQ	Transf erase; Kinase; Complete_proteome.	Db	214 CAIRAGKSNT 224
SEQUENCE	397 AA; 43115 MW; 502254AEF92CBF51 CRC64;	RESULT 7	YNV5_CABEL STANDARD; PRT; 451 AA.
DR	ACK2_LISMO	ID YNV5_CABEL	AC P34568;
DR	STANDARD; PRT; 397 AA.	DT 01-FEB-1994 (Rel. 28, Created)	DE Hypothetical protein TI6H12.5 in chromosome III.
Qy	1 CASELGKSTNT 11	RN [1]	GN TI6H12.5.
DB	214 CAIRAGKSNT 224	RN [2]	OS Caenorhabditis elegans.
DR	ACK2_LISMO	RN [3]	OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
DR	STANDARD; PRT; 397 AA.	RN [4]	OC Rhabditidae; Pelderinae; Caenorhabditis.
DR	28-FEB-2003 (Rel. 41, Created)	RN [5]	NCBI_TaxID=6239;
DR	28-FEB-2003 (Rel. 41, Last sequence update)	RN [6]	SEQUENCE FROM N.A.
DR	Acetate Kinase 2 (EC 2.7.2.1) (Acetokinase 2).	RN [7]	SPRAIN-Bristol N2;
DR	ACK2 OR LM01168.	RN [8]	RA Smith A.; RA Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
OS	Listeria monocytogenes.	RN [9]	RA Durbin R.; RA Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
OC	Bacterium; Firmicutes; Bacillales; Listeriaceae; Listeria.	RJ [10]	CC -1- SIMILARITY: Contains 1 MATH domain.
OX	NCBI_TaxID=1639;	RJ [11]	CC -1- SIMILARITY: Contains 1 BTB/POZ domain.
RP	SEQUENCE FROM N.A.	CC [12]	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RC	STRAINEGD-e / Serovar 1/2a; MEDLINE=21537279; PubMed=11679660;	CC [13]	CC [14]
RX	Glaser P., Prangeul L., Buchrieser C., Rusniok C., Amend A.,	CC [15]	CC [16]
RA	Baquero F., Berche P., Blococker H., Brandt P., Chakrabortty T.,	CC [17]	CC [18]
RA	Charbito F., Chetouani F., Couve E., de Darvur A., Dehoux P.,	CC [19]	CC [20]
RA	Domann B., Dominguez-Bernal G., Duchaud E., Durant L., Dussurgeot O.,	CC [21]	CC [22]
RA	Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,	CC [23]	CC [24]
RA	Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,	CC [25]	CC [26]
RA	Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,	CC [27]	CC [28]
RA	Madueno E., Maitouroun A., Mata Vicente J., NG E., Nedjari H.,	CC [29]	CC [30]
RA	Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,	CC [31]	CC [32]
RA	Remmeli B., Rose M., Schlueter T., Simoes N., Tierrez A.,	CC [33]	CC [34]
RA	Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,	CC [35]	CC [36]
RT	"Comparative genomics of Listeria species.";	CC [37]	CC [38]
RL	Science 94:849-852 (2001).	CC [39]	CC [40]
CC	-!- CATALYTIC ACTIVITY: ATP + acetate = ADP + acetyl phosphate.	CC [41]	CC [42]
CC	-!- PATHWAY: Conversion of acetate to acetyl-CoA; First step.	CC [43]	CC [44]
CC	-!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).	CC [45]	CC [46]
CC	-!- SIMILARITY: Belongs to the acetokinase family.	CC [47]	CC [48]
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC [49]	CC [50]
DR	EMBL; AL591978; CAC99246..1;	Query Match	54.2%; Score 39; DB 1; Length 451;
DR	PIR; AH1220; AH1220.	Best Local Similarity	58.3%; Pred. No. 14;
DR	ListiList; LIN001168; -.	Matches	7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
DR	HAMAP; MF 00020; ..1.	Qy	1 CASELGKSTNT 12
DR	InterPro; IPR000890; Acetate_kin.	Db	271 CKSDLGSPQTIF 282

RESULT 8

IL1F9_HUMAN STANDARD; PRT; 169 AA.

AC Q9NZE8; (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Interleukin 1 family member 9 (IL-1F9) (Interleukin-1 homolog 1) (IL-1H1) (Interleukin-1 epsilon) (IL-1 epsilon) (IL-1 related protein 2) (IL-1RP2).

DE NCBITaxonID=9606;

GN IL1F9 OR IL1H1 OR IL1E OR IL1RP2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX [1]

RN RP SEQUENCE FROM N.A.

RC TISSUE=Keratinocytes;

RA Kumaz S., McDonnell P.C., Lehr R., Tierney L., Trizmas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L., Young P.R.;

RA "Identification and initial characterization of four novel members of the interleukin-1 family"; RT J. Biol. Chem. 275:10308-10314 (2000).

[2] RN SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC TISSUE=Epithelium;

RA MEDLINE=21359532; PubMed=11466363;

RA Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S., Wagner J., Edwards G., Clifford T., Menon S., Baran J.F., Kascelin R.A.; RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kappa B activation through the orphan IL-1 receptor-related protein 2.";

RA J. Immunol. 167:1440-1446(2001).

[3] RN SEQUENCE FROM N.A.

RA MEDLINE=20318623; PubMed=10860666;

RA Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S., Zhou H., Leiby K.B., Holmgren L.M., Gearing D.P., Pan Y., RT "Identification and gene organization of three novel members of the IL-1 family on human chromosome 2.";

RA Genomics 62:213-216 (2000).

-!- FUNCTION: Function as an agonist of NF-kappa B activation through the orphan IL-1 receptor-related protein 2. Could constitute part of an independent signaling system analogous to interleukin-1 alpha (IL-1A), beta (IL-1B) receptor agonist and interleukin-1 receptor type 1 (IL-1R1), that is present in epithelial barriers and takes part in local inflammatory response.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Highly expressed in tissues containing epithelial cells: skin, lung, stomach and esophagus. In skin is expressed only in keratinocytes but not in fibroblasts, endothelial cells or melanocytes. Up-regulated in lesional psoriasis skin.

-!- INDUCTION: By TNF-alpha and by IFN-gamma in keratinocytes.

-!- SIMILARITY: Belongs to the IL-1 family.

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DR DR MIM; 605542; -; P; cell-cell signaling; TAS

DR GO; GO:0007267; P; response to pest/pathogen; parasite; TAS

DR InterPro; IPR009633; P; cytok IL1-like.

DR InterPro; IPR000975; Interleukin_1.

DR Pfam; PF00340; IL1; 1.

DR SMART; SM00125; INTERLEUKIN_1; FALSE NEG.

DR PROSITE; PS00253; INTERLEUKIN_1; FALSE NEG.

KW Cytokine; Multigene family.

SEQUENCE 169 AA; 18721 MW; F00A924370674154 CRC64;

Query Match 51.4%; Score 37; DB 1; Length 169;

Best Local Similarity 88.9%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SELGKSTNT 11

Db 153 SELGKSYNT 161

RESULT 9

ISPH_BUCAI STANDARD; PRT; 319 AA.

ID ISPH_BUCAI

AC P57247;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2).

GN ISPH OR LYTB OR BU147.

OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) symbiotic bacteria.

OS Bacteroides; Proteobacteria; Gammaproteobacteria; Enterobactiales; Enterobactericeae; Buchnera.

NCBI_TaxID=118099;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Tokyo 1998;

RX MEDLINE=20445173; PubMed=10993077;

RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; RT Genome sequence of the endocellular bacterial symbiont of aphids

RT Buchnera sp. APS."

RL Nature 407:81-86 (2000).

CC -!- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP). (By similarity).

CC -!- CATALYTIC ACTIVITY: Isopentenyl diphosphate + NAD(P)(+) + H(2)O = (B)-4-hydroxy-3-methylbut-2-en-1-yl diphosphate + NAD(P)H.

CC -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh (1st) Step.

CC -!- SIMILARITY: Belongs to the isph family.

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CC DR EMBL; AP001118; BAB12865.1; -.

CC DR HAMAP; MF_00191; -; 1.

CC DR InterPro; IPR003451; LytB.

CC DR PF02401; PF02401; LYTB.

CC DR TIGRFAMS; TIGR00216; ISPH_lytB; 1.

CC KW Isoprene biosynthesis; Complete proteome; Oxidoreductase; NADP.

CC SEQUENCE 319 AA; 35741 MW; 69BAFCC12DD09B8 CRC64;

Query Match 51.4%; Score 37; DB 1; Length 319;

Best Local Similarity 70.0%; Pred. No. 23;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SELGKSTNTF 12

Matches	6;	Conservative	1;	Mismatches	6;	Indels	0;	Gaps	0;				
Qy	1 CASELIGKSTNTFC 13 : : 94 CKGHILGQPLNIFC 106												
Db													
RESULT 11													
PMBB_ERWCH	PMBB_ERWCH	STANDARD;	PRT;	433 AA.									
AC	Q47474;												
DT	01-NOV-1997 (Rel. 35, Created)												
DT	01-NOV-1997 (Rel. 35, Last sequence update)												
DT	10-OCT-2003 (Rel. 42, Last annotation update)												
DE	Pectinesterase B precursor (EC 3.1.1.11) (Pectin methylesterase B)												
DE	(PE B).												
GN	PEMB.												
OS	Erwinia chrysanthemi.												
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales;												
NCBI_TAXID	556;												
RN	[1]												
RP	SEQUENCE FROM N.A.												
RC	STRAIN=937;												
RX	MEDLINE=937;												
RX	MEDLINE=96228695; PubMed=8830237;												
RA	Shevchik V.E., Condemine G., Hugouvieux-Cotte-Pattat N.,												
RA	Robert-Baudouy J.												
RR	"Characterization of pectin methyl esterase B, an outer membrane												
RR	lipoprotein of Erwinia chrysanthemi 3937.";												
RT	Mol. Microbiol. 19:455-466(1996).												
RL	-!- FUNCTION: PROBABLY INVOLVED IN THE DEGRADATION OF METHYLATED												
CC	OLIGOGALACTURONIDES PRESENT IN THE PERIPLASM.												
CC	-!- CATALYTIC ACTIVITY: Pectin + N H ₂ O = N methanol + pectate.												
CC	-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid												
CC	ANCHOR.												
CC	-!- INDUCTION: By pectin.												
CC	-!- SIMILARITY: Belongs to the pectinesterase family.												
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration												
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CC	the European Bioinformatics Institute. There are no restrictions on its												
CC	use by non-profit institutions as long as its content is in no way												
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/												
CC	or send an email to license@isb-sib.ch).												
CC	-----												
DR	X84665; CA59151.L; -												
DR	PIR; S70914; S70914.												
DR	InterPro; IPR000070; Pectinesterase.												
PFam	PF0095; Pectinesterase_1.												
DR	PROSITE; PS00800; PECTINESTERASE_1.												
DR	PROSITE; PS00503; PECTINESTERASE_2.												
KW	Hydrolase; Aspartyl esterase; Outer membrane; Lipoprotein; Signal;												
KW	Palmitate.												
FT	SIGNAL 1 21												
FT	CHAIN 22 433												
FT	LIPID 22 22												
FT	ACT SITE 22 259												
FT	ACT SITE 292 292												
SQ	SEQUENCE 433 AA; 46793 MW;												
Query Match	51.4%; Score 37; DB 1; Length 433;												
Best Local Similarity	46.2%; Pred. No. 32;												
Matches	6; Conservative 3;												
Qy	1 CASELIGKSTNTFC 13 : : 192 CATKAGTRINTC 204												
Db													

RESULT 12
PK1_SCHPO

RESULT 12
PK1_SCHPO

PCKL_SCHPO STANDARD; PRT; 988 AA.
ID P3582; AC P3582; DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C-like 1 (EC 2.7.1.-).
GN PK1 OR SPAC7G8.14C OR SPAC22H10.01C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomyces;
OC Schizosaccharomyctales; Schizosaccharomyctaceae.
OC Schizosaccharomyces.
NCBI_TAXID=4996;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=1848401; PubMed=1859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feitwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Hollroyd S., Hornsby T., Howarth S., Hucke B.J., Hunt S., Jigges K.,
RA James K., Jones L., Lester S., McDonald S., McLean J.,
RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitz E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens S., Warren K., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Gromoprez B.,
RA Weltjens I., Vanstreels E., Holzer M., Scheffer M., Mueller Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler R., Wambutt R., Purnelle B.,
RA Goffeau E., Cadieu E., Dreano S., Gloux S., Lejaire V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillard C., Tallada V.A., Gazzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J.C., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Porschburg S.L.,
RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Nurse P.;
RA Shpakovski G.V., Ussey D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RN Nature 415:871-880(2002).
CC -!- FUNCTION: Involved in the control of the cell shape. Target
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. PKC
CC subfamily.
CC -----

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CC DR D14337; BAA0267.1; -
CC DR EMBL; 269710; CAA93602.1; -
CC DR EMBL; 269795; CAA93697.1; -
CC DR HSSP; Q63450; 1A06.
DR GeneDB_Spombe; SPAC17G8.14C; -
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CalB.
DR InterPro; IPR002219; DAG_Pe-bind.
DR InterPro; IPR000961; Kinase_C.

DR	InterPro; IPR000719; Prot_kinase.	DR	HSSP; Q63450; 1A06.
DR	InterPro; IPR000861; REM_repeat.	DR	InterPro; IPR000008; C2.
DR	InterPro; IPR008271; Ser_thr_Pkinase.	DR	InterPro; IPR08973; C2_CalB.
DR	Pfam; PF00168; C2_1.	DR	InterPro; IPR002219; DAG_PeBind.
DR	Pfam; PF00130; DAG_Pe-bind; 2.	DR	InterPro; IPR000961; Pkinase_C.
DR	Pfam; PF02185; HR1_2.	DR	InterPro; IPR00719; Prot_Kinase.
DR	Pfam; PF00069; Pkinase_1.	DR	InterPro; IPR00851; REM_Repeat.
DR	Pfam; PF00433; Pkinase_C_1.	DR	InterPro; IPR008271; Ser_thr_Pkinase.
DR	ProDom; PD000001; Prot_Kinase; 1.	DR	InterPro; IPR02390; Ser_thr_Pkinase.
DR	SMART; SM00130; CL_2.	DR	Pfam; PF00130; DAG_PeBind; 2.
DR	SMART; SM00239; C2_1.	DR	Pfam; PF02185; HR1_2.
DR	SMART; SM00074; HR1_2.	DR	Pfam; PF00069; Pkinase_1.
DR	SMART; SM00133; S_TK_X; 1.	DR	Prodom; PD000001; Prot_Kinase; 1.
DR	SMART; SM00220; S_TKC; 1.	DR	SMART; SM00109; CL_2.
DR	PROSITE; PS00479; DAG_Pe_BIND_DOM_1_2.	DR	SMART; SM00239; C2_1.
DR	PROSITE; PS00081; DAG_Pe_BIND_DOM_2_2.	DR	SMART; SM00074; HR1_2.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	DR	SMART; SM00220; S_TKC_X; 1.
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.	DR	PROSITE; PS00479; DAG_Pe_BIND_DOM_1_2.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Zinc;	DR	PROSITE; PS00091; DAG_Pe_BIND_DOM_2_2.
KW	Phorbol-ester binding; Repeat.	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
FT	DOMAIN 414 461 PHORBOL-ESTER AND DAG BINDING 1.	DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
FT	DOMAIN 481 530 PHORBOL-ESTER AND DAG BINDING 2.	DR	PROSITE; PS00018; PROTEIN_KINASE_ST; 1.
FT	DOMAIN 664 923 PROTEIN_KINASE.	KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Zinc;
FT	NP_BIND 670 678 ATP (BY SIMILARITY).	KW	Phorbol-ester binding; Repeat.
FT	BINDING 693 693 ATP (BY SIMILARITY).	FT	DOMAIN 459 506 PHORBOL-ESTER AND DAG BINDING 1.
FT	ACT SITE 789 789 BY SIMILARITY.	FT	DOMAIN 527 576 PHORBOL-ESTER AND DAG BINDING 2.
FT	CONFFLICT 27 35 AMYGDALIN -> SNGGPDGES (IN REF. 1).	FT	DOMAIN 704 709 POLY-ALA.
SQ	SEQUENCE 988 AA; 111783 MW; 0969DEC1AB43C4E CRC64;	FT	DOMAIN 785 792 POLY-PRO.
Query Match	Best Local Similarity 51.4%; Score 37; DB 1; Length 988;	FT	DOMAIN 849 1108 PROTEIN_KINASE.
Matches	6; Conservative 66.7%; Pred. No. 73; Indels 0; Gaps 0;	FT	NP_BIND 855 863 ATP (BY SIMILARITY).
SQ	5 LGKSTNTFC 13	FT	BINDING 878 878 ATP (BY SIMILARITY).
Db	817 LGNTTSTFC 825	FT	ACT SITE 974 1174 AA; 130506 MW; 264ADD42849F37C CRC64;
Query Match	51.4%; Score 37; DB 1; Length 1174;	Matches	7; Conservative 46.7%; Pred. No. 87;
Best Local Similarity	51.4%; Score 37; DB 1; Length 988;	Mismatches	3; Mismatches 3; Indels 2; Gaps 1;
Matches	6; Conservative 66.7%; Pred. No. 73; Indels 0; Gaps 0;	SQ	1 CASEL--GKSNTFC 13
Qy	5 LGKSTNTFC 13	Db	996 CKEEMWGSTIFC 1010
RESULT 13		RESULT 14	
KPC1_COCHE	ID KPC1_COCHE STANDARD; PRT; 1174 AA.	YOH5_YEAST	YOH5_YEAST STANDARD; PRT; 1294 AA.
AC 042632;	AC Q08233; Q08233; PRT; 1294 AA.	AC Q08233; Q08233; PRT; 1294 AA.	AC Q08233; Q08233; PRT; 1294 AA.
DT 15-JUL-1999 (Rel. 38, Created)	DT 01-NOV-1997 (Rel. 35, Created)	DT 01-NOV-1997 (Rel. 35, Created)	DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)	DT 16-OCT-2001 (Rel. 40, Last sequence update)	DT 16-OCT-2001 (Rel. 40, Last sequence update)	DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Protein kinase C-like (EC 2.7.1.-).	DE Probable ATP-dependent transporter YOL074C/YOL075C.	DE Probable ATP-dependent transporter YOL074C/YOL075C.	DE Probable ATP-dependent transporter YOL074C/YOL075C.
GN	NCBI_TaxID=5016;	GN YOL074C/YOL075C	GN YOL074C/YOL075C
OS Cochliobolus heterostrophus (Drechslera maydis). Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pileosporaceae; Cochliobolus.	OS Saccharomyces cerevisiae (Baker's yeast).	OS Saccharomyces cerevisiae (Baker's yeast).	OS Saccharomyces cerevisiae (Baker's yeast).
NCBI_TaxID=5016;	NCBI_TaxID=5016;	NCBI_TaxID=5016;	NCBI_TaxID=5016;
RN		RN	RN
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 48329 / C2;	RC Tzermia M., Katsoulou C.; Alexandraki D.;	RC Tzermia M., Katsoulou C.; Alexandraki D.;	RC Tzermia M., Katsoulou C.; Alexandraki D.;
RA Oser B.M., Yoder O.C.;	RA "Sequence analysis of a 33.2 kb segment from the left arm of yeast chromosome XV reveals eight known genes and ten new open reading frames including homologues of ABC transporters, inositol phosphatases and human expressed sequence tags."	RA "Sequence analysis of a 33.2 kb segment from the left arm of yeast chromosome XV reveals eight known genes and ten new open reading frames including homologues of ABC transporters, inositol phosphatases and human expressed sequence tags."	RA "Sequence analysis of a 33.2 kb segment from the left arm of yeast chromosome XV reveals eight known genes and ten new open reading frames including homologues of ABC transporters, inositol phosphatases and human expressed sequence tags."
RL PROBABILITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.	RL Yeast 13:593-599 (1997).	RL Yeast 13:593-599 (1997).	RL Yeast 13:593-599 (1997).
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. PKC subfamily.	CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).	CC -!- SUBCELLULAR LOCATION: Belongs to the ABC transporter family. MDR subfamily.	CC -!- SUBCELLULAR LOCATION: Belongs to the ABC transporter family. MDR subfamily.
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CC DR Y15839; CRA75801.1; -.	CC DR PIR; T43051; T43051.	CC DR PIR; T43051; T43051.	CC DR PIR; T43051; T43051.

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```
CC EMBL; Z74817; CAA9085.1; -
DR EMBL; Z74816; CAA9084.1; -
DR PIR; S77690; S77690.
DR GerOnline; 143497;
DR SGD; S0005435; YOLO75C.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003430; ABC transporter.
DR Pfam; PF00005; ABC tran; 2.
DR ProDom; PD000006; ABC transporter; 2.
DR SMART; SM0388; AAA; 2.
DR PROSITE; PS00211; ABC TRANSPORTER_1; 2.
DR PROSITE; PS50893; ABC TRANSPORTER_2; 2.
DR Hypothetical protein; ATP-binding; Transmembrane; Glycoprotein;
KW Transport; Repeat.
FT TRANSMEM 376 396 POTENTIAL.
FT TRANSMEM 496 516 POTENTIAL.
FT TRANSMEM 531 551 POTENTIAL.
FT TRANSMEM 605 625 POTENTIAL.
FT TRANSMEM 1039 1059 POTENTIAL.
FT TRANSMEM 1121 1141 POTENTIAL.
FT TRANSMEM 1267 1287 POTENTIAL.
FT NP_BIND 62 69 ATP (POTENTIAL).
FT NP_BIND 727 734 ATP (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 341 341 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 349 349 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 528 528 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 983 983 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1062 1062 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1294 AA; 145157 MW; C555500A45B5284E CRC54;
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Query Match Score 37; DB 1; Length 1294;
Best Local Similarity 58.3%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy 1 CASELGKSTNTFC 12
Db 1161 CGERLGIMTNTF 1172
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RESULT 15
UL16_HCMVA STANDARD; PRT; 230 AA.
TD _UL16_HCMVA
AC P16757;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Hypothetical protein UL16.
GN UL16.
OS Human cytomegalovirus (strain AD169).
CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC Betaherpesvirinae; Cytomegalovirus.
CX NCBI_TAXID=10360;
RN [1] _TAXID=10360;
RP SEQUENCE FROM N_A.
RX MEDLINE=90269039; PubMed=2161319;
RA Chee M.S., Bantick A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchinson C.A., III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; "Analysis of the Protein-coding content of the sequence of human cytomegalovirus strain AD169";
RT Curr. Top. Microbiol. Immunol. 154:125-169 (1990).
```

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```
CC DR; X17403; CAA35448.1; -
DR PTR; S09778; S09778.
KW Hypothetical protein.
FT CARBOHYD 35 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 41 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 68 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 101 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 145 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 230 AA; 26147 MW; B72F2C241C569967 CRC64;
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Query Match Score 36.5; DB 1; Length 230;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
Job time : 7.90909 secs
Qy 1 CASELG-KSTNTFC 13
Db 25 CAVIDGSKSSNNTC 38
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Search completed: September 5, 2004, 09:56:01

Result No.	Score	Query	Match Length	DB ID	Description	Summary
1	51	Q91ZB4	326	1	Q91ZB4 rattus norvegicus	
2	49	Q91ZB4	127	13	Q91ZB4 rana pipiens	
3	43	Q91ZB4	127	13	Q91ZB4 rana pipiens	
4	43	Q91ZB4	997	5	Q91ZB4 trypanosoma brucei	
5	42	Q91ZB4	1011	3	Q91ZB4 pneumocystis jirovecii	
6	41	Q91ZB4	316	13	Q91ZB4 brachydanio rerio	
7	40	Q91ZB4	283	16	Q91ZB4 rhodopirellus	
8	40	Q91ZB4	383	12	Q91ZB4 parametrio	
9	40	Q91ZB4	605	16	Q91ZB4 bacillus anatum	
10	40	Q91ZB4	605	16	Q91ZB4 cryptosporidium	
11	39.5	Q91ZB4	621	5	Q91ZB4 rana catesbeiana	
12	39	Q91ZB4	128	13	Q91ZB4 lactobacillus	
13	39	Q91ZB4	471	10	Q91ZB4 arabinopsis	
14	39	Q91ZB4	677	10	Q91ZB4 arabinopsis	
15	39	Q91ZB4	738	10	Q91ZB4 arabinopsis	
16	39	Q91ZB4	1117	10	Q91ZB4 arabinopsis	
17	39	Q91ZB4	542	5	Q91ZB4 plasmidium	
18	38	Q91ZB4	528	2	Q91ZB4	
19	38	Q91ZB4	528	2	Q91ZB4	
20	38	Q91ZB4	528	49	Q91ZB4	
21	38	Q91ZB4	528	13	Q91ZB4	
22	38	Q91ZB4	528	15	Q91ZB4	
23	38	Q91ZB4	528	15	Q91ZB4	
24	38	Q91ZB4	528	15	Q91ZB4	
25	38	Q91ZB4	528	15	Q91ZB4	
26	38	Q91ZB4	528	16	Q91ZB4	
27	38	Q91ZB4	528	16	Q91ZB4	
28	38	Q91ZB4	528	15	Q91ZB4	
29	38	Q91ZB4	528	15	Q91ZB4	
30	38	Q91ZB4	528	15	Q91ZB4	
31	38	Q91ZB4	528	15	Q91ZB4	
32	38	Q91ZB4	528	15	Q91ZB4	
33	38	Q91ZB4	528	15	Q91ZB4	
34	38	Q91ZB4	528	15	Q91ZB4	
35	38	Q91ZB4	528	15	Q91ZB4	
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40	38	Q91ZB4	528	15	Q91ZB4	
41	38	Q91ZB4	528	15	Q91ZB4	
42	38	Q91ZB4	528	15	Q91ZB4	
43	38	Q91ZB4	528	15	Q91ZB4	
44	38	Q91ZB4	528	15	Q91ZB4	
45	38	Q91ZB4	528	16	Q91ZB4	

Db	126 ASEEGKTTNTFP	136	DR PROSITE; PS00127; RNASE_PANCREATIC; 1. KW SIGNAL; 23 FT 1 AA; 14469 MW; SQ 127 AA;
RESULT 2			
Q9I8V8	PRELIMINARY;	PRT;	127 AA.
ID Q9I8V8;			
AC Q9I8V8;			
DR 01-OCT-2000 (TREMBLrel. 15, Created)			
DR 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DR 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Onconase variant rapLR1 precursor.			
OS Rana pipiens (Northern leopard frog).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.			
OC NCBI_TAXID=8404;			
RN [1]			
SEQUENCE FROM N.A.			
RC TISSUE=liver			
RX MEDLINE=20330357; PubMed=10871370;			
RX RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.; "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a 3' UTR of unusual length and structure."; RPI Nucleic Acids Res. 2000; 28:2375-2382 (2000).			
RT DR EMBL; AF65113; AA176935.1; -.			
RT DR PIR; A39035; A39035.			
DR HSSP; P22069; IONC.			
DR GO; GO:0003676; F:nucleic acid binding; IEA.			
DR GO; GO:004522; F:pancreatic ribonuclease activity; IEA.			
DR InterPro; IPR001422; RNaseA.			
DR Pfam; PF00074; rnaseA_1.			
DR ProDom; PD00035; rnaseA_1.			
DR SMART; SM00929; RNASE_Pc_1.			
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.			
DR SIGNAL.			
FT SIGNAL.	1	23	POTENTIAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;			
Query Match 68.1%; Score 49; DB 13; Length 127; Best Local Similarity 69.2%; Pred. No. 0.26; Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0; KW Signal.			
Qy 1 CASELGKSTNTFC 13			
Db 98 CXYKLKSTNTFC 110			
RESULT 3			
Q8UYX5	PRELIMINARY;	PRT;	127 AA.
ID Q8UYX5			
AC Q8UYX5;			
DR 01-MAR-2002 (TREMBLrel. 20, Created)			
DR 01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DR 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Onconase precursor.			
GN RPI.			
OS Rana pipiens (Northern leopard frog).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.			
OC NCBI_TAXID=8404;			
RN [1]			
SEQUENCE FROM N.A.			
RC Liao Y.-D., Wang S.-C.; "Rana pipiens onconase genomic DNA."; Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases			
RC EMBL; AF332139; AAL54383.1; -.			
DR PIR; A39035; A39035.			
DR GO; GO:0003676; F:nucleic acid binding; IEA.			
DR InterPro; IPR01427; RNaseA.			
DR Pfam; PF00074; rnaseA_1.			
DR ProDom; PD000535; RNaseA_1.			
DR SMART; SM00929; RNASE_Pc_1.			
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.			
DR DBFDC3D8D2642A3 CRC64;			
Query Match 59.7%; Score 43; DB 5; Length 99; Best Local Similarity 58.3%; Pred. No. 3.0; Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;			
Qy 1 CASELGKSTNTFC 12			
Db 460 CGSKRGRTNTFC 471			
RESULT 5			
Q9P944	PRELIMINARY;	PRT;	1011 AA.
ID Q9P944			
AC Q9P944;			
DR 01-OCT-2000 (TREMBLrel. 15, Created)			
DR 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DE Kexin-like protease KEX1.			
GN KEX1.			
OS Pneumocystis carinii f. sp. muris.			
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidae;			
OC Pneumocystis.			
DR NCBI_TAXID=42066;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=20184731; PubMed=10721706;			

Lee L.H., Gigliotti F., Wright T.W., Simpson-Haidaris P.J., Weinberg G.A., Haidaris C.G.; "Molecular characterization of Kex1, a kexin-like protease in mouse Pneumocystis carinii"; Gene 24(2):141-150 (2000).

-!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.

DR EMBL; AF093132; AAF32493.1; -.

DR GO; GO:0008233; F-peptidase activity; IEA.

DR GO; GO:0004283; F-subtilase activity; IEA.

DR GO; GO:0006508; P-protease and peptidolysis; IEA.

DR InterPro; IPR000239; Peptidase_S8.

DR InterPro; IPR002844; Peptidase_S8B.

DR InterPro; IPR006590; PT.

DR InterPro; IPR002955; P-rich extensin.

DR PFAM; PF00082; Peptidase_SP; 1.

DR PFAM; PF04886; PT; 4.

DR PFAM; PF01483; P-protein; 1.

DR PRINTS; PRO1217; ERICHEXTENIN.

DR PRINTS; PRO00723; SUBTILLISIN.

DR ProdDom; PD00017; P-domain; 1.

DR PROSITE; PS00137; SUBTILASE_HIS; 1.

KW Protease.

SQ SEQUENCE: 1011 AA; 112021 MW; FBE4122CF865864E8 CRC64;

Query Match 58.3%; Score 42; DB 3; Length 1011;

Best Local Similarity 53.8%; Prod. No. 48; Gaps 0;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CASBLGKSTNTFC 13
[1]: : |||
Db 246 CAGTEVAAKNTFC 258

RESULT 6

Q902B2 ID PRELIMINARY; PRT; 316 AA.

AC DT 01-DEC-2001 (TREMBLrel. 19, Created)

CC DT 01-JUN-2003 (TREMBLrel. 19, Last sequence update)

DR DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE DE Transcript factor Gbx1.

GN OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

RN NCBI_TaxID:7955;

RP SEQUENCE FROM N.A.

RA Lun K., Thisse C., Amores A., Yan Y., Postlethwait J., Brand M.; "Gbx2 but not gbx1 is dependent on fgf8 function"; Submitted (JUL 2000) to the ENSEMBL/GenBank/NCBI databases.

RL -!- SUBCELLULAR LOCALIZATION: NUCLEAR (BY SIMILARITY).

CC DR EMBL; AF228763; AAC83070.1; -.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0006355; P:regulation of transcription, factor activity; IEA.

DR InterPro; IPR001356; Homeobox.

DR PRINTS; PRO00024; HOMEOBOX.

DR ProdDom; PB000010; Homeobox; 1.

DR PROSITE; SM00389; HOX; 1.

DR PROSITE; PS00027; HOMEBOX_1; 1.

DR PROSITE; PS50071; HOMEBOX_2; 1.

KW DNA-binding; Homeobox; Nuclear protein.

SQ SEQUENCE: 316 AA; 34408 MW; DC32955EA5430D8A CRC64;

Query Match 56.9%; Score 41; DB 13; Length 316;

Best Local Similarity 66.7%; Prod. No. 22;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RT	PBCV-1.";	DR	InterPro; IPR001567; Peptidase_M3.
RL	virology 276:27-36 (2000).	DR	InterPro; IPR006025; Pept_M_Zn_BS.
RN	[4]	DR	Pfam; PF0132; Peptidase_M3_1_-
RP	SEQUENCE FROM N.A.	DR	PROSITE; PS01042; ZINC_PROTEASE; 1.
RA	Van Etten J.L.'s	KW	Complete proteome.
RA	Submitted (DDBJ-1995) to the EMBL/GenBank/DBJ databases.	SEQUENCE	605 AA; 69285 MW; 138E401597519248 CRC64;
RN	[5]	Query	Match 55.6%; Score 40; DB 16; Length 605;
RP	SEQUENCE FROM N.A.	Best Local Similarity 58.3%; Pred. No. 67;	
RA	Van Etten J.L.'s	Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	
RA	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.	QY	2 ASELGKSTNTFC 13
RN	[6]	Db	358 ADNGKSTGAFC 369
RP	SEQUENCE FROM N.A.	RESULT 1.0	
RA	Van Etten J.L.'s	OB1410 PRELIMINARY; PRT; 605 AA.	
RA	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.	ID	Q81410
RN	[7]	AC	Q81410; 24. Created)
RP	SEQUENCE FROM N.A.	DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
RA	Graves M.V.'s Van Etten J.L.'	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
RA	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.	DE	Oligoendopeptidase F (EC 3.4.24.-).
RN	[8]	GN	BC453.
RP	SEQUENCE FROM N.A.	OS	Bacillus cereus (strain ATCC 14579 / DSM 31).
RA	Graves M.V.'s Van Etten J.L.'	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
RA	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.	OX	NCBI_TaxID=226900;
RN	[9]	RP	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RX	MEDLINE:22606415; PubMed=12721630;
RA	Gurtin J.R.'s Graves M.V.'s Van Etten J.L.'	RA	Ivanova N., Sorokin A., Anderson T., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyripides N.; "Genome sequence of <i>Bacillus cereus</i> and comparative analysis with <i>Bacillus anthracis</i> ," Nature 423:87-91 (2003).
RA	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.	DR	EMBL; AE01705; AAP12314.1; -
DR	U32580; AAC6599.1; -	DR	GO; GO:0016787; F:hydrolase activity; IEA.
PIR	T17722; T17722.	DR	DR; GO:0004222; F:metalloendopeptidase activity; IEA.
SQ	SEQUENCE 383 AA; 43643 MW; B04E602D99973DCF CRC64;	DR	GO; GO:0008270; F:zinc ion binding; IEA.
Query	55.6%; Score 40; DB 12; Length 383;	DR	DR; GO:0006508; P:proteolysis and peptidolysis; IEA.
Best Local Similarity 46.2%; Pred. No. 42;	Best Local Similarity 46.2%; Pred. No. 42;	DR	DR; InterPro; IPR006025; Pept_M_Zn_BS.
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;	Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;	DR	PFAM; PF1432; Peptidase_M3_1.
QY	1 CASELGKSTNTFC 13	DR	PROSITE; PS00142; ZINC_PROTEASE; 1.
Db	304 CVMNIGKKNNEFC 316	KW	Hydrolase; Complete protein.
RESULT 9	SEQUENCE FROM N.A.	SEQUENCE	605 AA; 6923 MW; 3C16DB0B1B2F4062 CRC64;
OB141B	PRELIMINARY; PRT; 605 AA.	Query	Match 55.6%; Score 40; DB 16; Length 605;
AC	Q8141B; 24. Created)	Best Local Similarity 58.3%; Pred. No. 67;	
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)	Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	QY	2 ASELGKSTNTFC 13
DE	Oligoendopeptidase F, putative.	Db	358 ADNGKSTGAFC 369
GN	BA5706.	RESULT 11	
OS	Bacillus anthracis (strain Ames). Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	Q7YYH2	PRELIMINARY; PRT; 621 AA.
OX	NCBI_TaxID=198094;	ID	Q7YYH2
RN	SEQUENCE FROM N.A.	AC	-
RP	MEDLINE=2260814; PubMed=12721629;	DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)
RA	Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
RA	Holzapfel E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,	DE	F-box domain protein.
RA	Kolonay J.P., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,	GN	1MB_228.
RA	DeBoy R.T., Madupu R., Daugherty S.C., Eisen J.A., Gill S.R.,	OS	Cryptosporidium parvum.
RA	Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,	OC	Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimerida;
RA	Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,	OC	Cryptosporidiidae; Cryptosporidium.
RA	Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,	NCBI_TaxID=5807;	NCBI_TaxID=5807;
RA	Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,	DR	
RA	Thomaeson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,	TIGR; BA5706; -	
RA	Fraser C.M.;	DR; GO:0004222; F:metalloendopeptidase activity; IEA.	
RA	"The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria."	DR; GO: GO:0008270; F:zinc ion binding; IEA.	
RA	closely related bacteria."	DR; GO: GO:0005508; P:proteolysis and peptidolysis; IEA.	
RA	423:81-86 (2003).	DR; GO: GO:0005508; P:proteolysis and peptidolysis; IEA.	

DR 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical protein.

GN AT4G01400.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyt; Magnoliophyt; eudicots; rosids;

OC euroids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;

OX NCBI_TAXID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M.,

RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

RA Kim C., Lin J., Liu S.X., Narusawa M., Pham P.K., Sakano H.,

RA Sakura T., Satou M., Seki M., Shimizu F., Yamada K., Shinozaki K.,

RA Ecker J., Theologis A., Davis R.W.,

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY120763; AAN53321.1; -.

KW Hypothetical protein.

SEQUENCE 738 AA; 82977 MW; EFB1B0FDA7B15CE CRC64;

Query Match 54.2%; Score 39; DB 10; Length 738;

Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12

Db 543 CLSELGEISSTF 554

Search completed: September 5, 2004, 09:59:52
Job time : 31.4141 secs

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OM protein - protein search, using sw mode!

Run on: September 5, 2004, 09:37:49 ; Search time 42.6768 Seconds
 86.068 Million cell updates/sec

Title: US-09-761-636A-5
 Perfect score: 72
 Sequence: 1 CASEIGKSINTFC 13

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:
 Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04:
 1: GeneseqP1980s:
 2: GeneseqP1990s:
 3: GeneseqP2000s:
 4: GeneseqP2001s:
 5: GeneseqP2002s:
 6: GeneseqP2003as:
 7: GeneseqP2003bs:
 8: GeneseqP2004s:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	13	4 AAU04524	Aau04524 VEGF base
2	72	100.0	17	4 AAU04527	Aau04527 VEGF base
3	69	95.8	13	4 AAU04534	Aau04534 VEGF base
4	69	95.8	17	4 AAU04550	Aau04550 VEGF base
5	65	95.8	17	4 AAU04546	Aau04546 VEGF base
6	65	90.3	13	4 AAU04535	Aau04535 VEGF base
7	65	90.3	13	4 AAU04537	Aau04537 VEGF base
8	65	90.3	17	4 AAU04547	Aau04547 VEGF base
9	65	90.3	17	4 AAU04551	Aau04551 VEGF base
10	65	90.3	17	4 AAU04549	Aau04549 VEGF base
11	61	84.7	13	4 AAU04536	Aau04536 VEGF base
12	61	84.7	17	4 AAU04548	Aau04548 VEGF base
13	54	75.0	73	4 AAU04522	Aau04522 Human VEG
14	54	75.0	96	4 AAU04520	Aau04520 Human VEG
15	54	75.0	109	2 AAU04520	Aau04520 Human NVR
16	54	75.0	109	3 AAB11931	Aab11931 Human tru
17	54	75.0	109	6 ABB84621	Abb84621 Human wil
18	54	75.0	109	6 ABG73750	Abg73750 Human VEG
19	54	75.0	287	6 ABG73779	Abg73779 Human NVR
20	54	75.0	325	2 AAM53240	Aam53240 Homo sapi
21	54	75.0	325	4 AAY97572	Aay97572 Human VEG
22	54	75.0	354	2 AAW44293	Aaw44293 Human vas
23	54	75.0	354	2 AAW49036	Aaw49036 Human zve
24	54	75.0	354	2 AAW53241	Aaw53241 Homo sapi
25	54	75.0	354	3 AAB10649	Aab10649 Human VEG

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGF (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a

26	54	75.0	354	3 AAY70750	Human pre
27	54	75.0	354	3 AAY70983	Human vas
28	54	75.0	354	3 AAB29049	Human VEG
29	54	75.0	354	4 AAB37606	Human VEG
30	54	75.0	354	4 AAB70685	Human vas
31	54	75.0	354	4 AAY9773	Human VEG
32	54	75.0	354	4 AAU08441	Polypepti
33	54	75.0	354	5 ABC33055	Human vas
34	54	75.0	354	5 ABG32046	Human Fit
35	54	75.0	354	6 ABB84623	Human VEG
36	54	75.0	354	7 ADD08950	Human VEG
37	54	75.0	620	2 AAM14994	c-F
38	51	70.8	110	5 AAM47933	Mouse VEG
39	51	70.8	178	2 AAY08287	Human gro
40	51	70.8	321	2 AAV53243	Mus muscu
41	51	70.8	321	5 AAM47931	Mouse VEG
42	51	70.8	326	2 AAW44296	Rat vascu
43	51	70.8	337	2 AAY08286	Human gro
44	51	70.8	358	2 AAM14992	Marine c-
45	51	70.8	358	2 AAW44295	Mouse vas

ALIGNMENTS

RESULT 1		AAU04524 standard; peptide; 13 AA.	
ID	AAU04524	XX	
AC	AAU04524;	XX	
DT	26-SEP-2001	(first entry)	
XX		DE	VEGF based monocyclic peptide 1.
		XX	Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequeiae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
		XX	Synthetic.
Key		FT	Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
XX		FT	
XX		PN	WO200152875-A1.
XX		PD	26-JUL-2001.
XX		PR	18-JAN-2001; 2001WO-US001533.
XX		PR	18-JAN-2000; 2000US-0176293P.
XX		PR	16-MAY-2000; 2000US-0204590P.
XX		PA	(LUDWIG INST CANCER RES.
XX		PA	Achen MG, Hughes RA, Stacker S, Cendron A,
XX		PI	WO200152875-A1.
XX		WPI	2001-442248/47.
XX		PT	Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
XX		PT	The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGF (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a

peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arteriopathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequaeae, hypertension induced neovascular sequaeae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy.

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) Sequence 13 AA;
Query Match      100.0%; Score 72; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
1 CASELGIKSTNTFC 13
1 CASELGIKSTNTFC 13
1 CASELGIKSTNTFC 13

```

RESULT 2
AAU04527 standard; protein, 17 AA.
AAU04527;
VEGF based bicyclic dimeric peptide #1.
Human; VEGF; vascular endothelial growth factor; angiogenesis;
neovascularisation; lymphangiogenesis; psoriasis; tumour;
diabetes induced neovascular sequelae; rheumatoid arthritis;
diabetic neuropathy; chronic inflammation; cyclic.

Key	Location/Qualifiers
Disulfide-bond	1..13 /note= "This bond cyclises the peptide"
Disulfide-bond	17 /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide, or to residue 1 of the sequence appearing as AAU04428, also forming a dimeric peptide."

WO200152875-A1.
26-JUL-2001.
18-JAN-2001; 2001WO-US0001533.
18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
(LUDWIG) LUDWIG INST CANCER RES.
Achen MG, Hughes RA, Stackler S

